

Hart, Edward

From: Swope, Sheridan
Sent: Friday, March 05, 2004 11:16 AM
To: Hart, Edward
Subject: FW: 09/966,880

Importance: High

Ed, the applicants have again made changes to the claims that require an additional search for this case (we're negotiating an allowance).

So, would you add the following to my rush search?
For 09/966,880, Pls search and interference search:

SID 7: full-length and oligo search (20NTs) against the NT data bases.

Thanks in advance for your great service!
Sheridan

[Swope, Sheridan] Sheridan Swope, Ph.D.
Patent Examiner, AU 1652
Recombinant Enzymes
571-272-0943 (voice)
E03A70 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

0574
3/5/04



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115892

TO: Sheridan Swope
Location: REM-3A70
Art Unit: 1652
Friday, March 05, 2004

Case Serial Number: 09/966880

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Swope,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 21:01:22 ; Search time 2776 Seconds

(without alignments)
9321.250 Million cell updates/sec

Title: US-09-966-880A-7_COPY_80_676

Perfect score: 597
Sequence: 1 atgacagccctcttgatgaa.....ctcgtactcttgagacttga 597

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 692750

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

GenBdb1:
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_on:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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15: em_ba:*
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17: em_hum:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	2.5	17	6	BD200908
2	15	2.5	20	6	AR298295
3	14	2.3	17	6	AX728573
4	14	2.3	17	6	AX759459
5	14	2.3	17	6	BD200909
6	14	2.3	20	6	AR026494
7	14	2.3	20	6	AR026495
8	14	2.3	20	6	AX487439
9	13	2.2	17	6	AX323965
10	13	2.2	17	6	AX323966
11	13	2.2	17	6	AX499488
12	13	2.2	17	6	AX499489
13	13	2.2	17	6	AX499490
14	13	2.2	17	6	AX499491
15	13	2.2	17	6	AX499492
16	13	2.2	17	6	AX673599
17	13	2.2	17	6	AX687581
18	13	2.2	17	6	AX687582
19	13	2.2	17	6	AX687583
20	13	2.2	17	6	AX687584
21	13	2.2	17	6	AX687585
22	13	2.2	17	6	AX735945
23	13	2.2	17	6	BD104902
24	13	2.2	19	6	AR241182
25	13	2.2	19	6	AR253259
26	13	2.2	19	6	AX129413
27	13	2.2	19	6	AX129414
28	13	2.2	19	6	AX259857
29	13	2.2	19	6	BD084645
30	13	2.2	20	4	DOCP43801
31	13	2.2	20	6	AR098868
32	13	2.2	20	6	I79708
33	13	2.2	20	6	AR257223
34	13	2.2	20	6	AR337175
35	13	2.2	20	6	AX428287
36	13	2.2	20	6	BD138115
37	12	2.0	13	6	AX358112
38	12	2.0	14	6	I43504
39	12	2.0	15	6	A09427
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41	12	2.0	15	6	A11578
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION BD200908 17 bp RNA linear PAT 17-JUL-2003
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD200908
VERSION BD200908.1 GI:33010678
KEYWORDS JP 2002509721-A/3934.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
Payco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
AUTHORS
TITLE Method and reagent for treating diseases or conditions concerning

JOURNAL molecule participating in vasculogenic response
 Patent: JP 2002509721-A 3934 02-APR-2002;
 RIBOZYME PHARMACEUTICALS INC
 OS Homo sapiens (human)
 PN JP 2002509721-A/3934
 PD 02-APR-2002
 PF 24-MAR-1999 JP 2000541291
 PR 27-MAR-1998 US 60/079678
 PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
 PI JAMES A MCSWIGGEN

PC C12N15/00,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
 A61P29/00,
 PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
 C12N5/00
 CC Method and reagent for treating diseases or conditions CC
 CC concerning molecule
 CC participating in vasculogenic response
 FH Key Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers

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 Location/Qualifiers
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QY 36 TTACCAATTCAAAA 50
 DB 1 TTACCAATTCAAAA 15

RESULT 2
 AR298295/c 20 bp DNA linear PAT 12-JUN-2003
 LOCUS AR298295
 DEFINITION Sequence 10030 from Patent US 6537751.
 ACCESSION AR298295
 VERSION AR298295.1 GI:31685579
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
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 source 1 (bases 1 to 20)
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REFERENCE
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 Patent: US 6537751-A 10030 25-MAR-2003;
 Location/Qualifiers
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QY 24 GAGGAAGTTCTTTA 38
 DB 15 GAGGAAGTTCTTTA 1

RESULT 3
 AX728573 17 bp DNA linear PAT 08-MAY-2003
 LOCUS AX728573
 DEFINITION Sequence 207 from Patent WO03025175.
 ACCESSION AX728573
 VERSION AX728573.1 GI:30507916

KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
 TITLE Sequences involved in phenomena of tumour suppression, tumour
 reversion, apoptosis and/or virus resistance and their use as
 medicines
 Patent: WO 03025175-A 207 27-MAR-2003;
 Molecular Engines Laboratories (FR)
 Location/Qualifiers
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 /db_xref="taxon:9606"

FEATURES

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QY 247 TCCTGAGCCCCCTG 260
 DB 3 TCCTGAGCCCCCTG 16

RESULT 4
 AX759499 17 bp DNA linear PAT 25-JUN-2003
 LOCUS AX759499
 DEFINITION Sequence 2820 from Patent WO03040369.
 ACCESSION AX759499
 VERSION AX759499.1 GI:32254115
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS Telerman,A., Anson,R. and Tuijinder,M.
 TITLE Sequences involved in tumoral suppression, tumoral reversion,
 apoptosis and/or viral resistance phenomena and their use as
 medicines
 Patent: WO 03040369-A 2820 15-MAY-2003;
 Molecular Engines Laboratories (FR)
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QY 422 TCAAGATTATTTT 435
 DB 3 TCAAGATTATTTT 16

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 BD200909 17 bp RNA linear PAT 17-JUN-2003
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 DEFINITION Method and reagent for treating diseases or conditions concerning
 molecule participating in vasculogenic response.
 ACCESSION BD200909
 VERSION BD200909.1 GI:33010679
 KEYWORDS JP 2002509721-A/3935.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 17)
AUTHORS Favco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 3935 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/3935
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PI 27-MAR-1998 US 60/079678
PI PAMELA A FAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT, JAMES A MCSWIGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC C12N5/00
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CC concerning molecule
CC participating in vasculogenic response
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FT /mol_type='genomic RNA'
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CY 37 TACCAATTCAAAA 50
DB 1 TACCAATTCAAAA 14
RESULT 6
LOCUS AR026494 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5856099.
ACCESSION AR026494
VERSION AR026494.1 GI:5937334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L., Bennett,C.Frank., Dean,N. and Geiger,T.
TITLE Antisense compositions and methods for modulating type I interleukin-1 receptor expression
JOURNAL Patent: US 5856099-A 1 05-JAN-1999;
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CY 373 GGGCTGGCGGCGCT 386
DB 7 GGGCTGGCGGCGCT 20
RESULT 7
LOCUS AR026495

LOCUS AR026495 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5856099.
ACCESSION AR026495
VERSION AR026495.1 GI:5937335
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Miraglia,L., Bennett,C.Frank., Dean,N. and Geiger,T.
TITLE Antisense compositions and methods for modulating type I interleukin-1 receptor expression
JOURNAL Patent: US 5856099-A 2 05-JAN-1999;
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LOCATION/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 373 GGGCTGGCGGCGCT 386
DB 2 GGGCTGGCGGCGCT 15
RESULT 8
LOCUS AX487439/c 20 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 4739 from Patent WO02053728.
ACCESSION AX487439
VERSION AX487439.1 GI:22321587
KEYWORDS
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE 1
AUTHORS Roemer,T., Jiang,B., Boone,C., Bussey,H. and Olsen,K.L.
TITLE Gene disruption methodologies for drug target discovery
JOURNAL Patent: WO 02053728-A 4739 11-JUL-2002;
Elitra Pharmaceuticals, Inc. (US)
FEATURES
LOCATION/Qualifiers
SOURCE 1..20
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CY 352 GACCGCAAGGCTGA 365
DB 14 GACCGCAAGGCTGA 1
RESULT 9
LOCUS AX323965/c 17 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 103 from Patent WO0192512.
ACCESSION AX323965
VERSION AX323965.1 GI:18094716
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
REFERENCE 1
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
 TITLE Targeted chromosomal genomic alterations in plants using modified
 single stranded oligonucleotides
 JOURNAL Patent: WO 0192512-A 103 06-DEC-2001;
 UNIVERSITY OF DELAWARE (US)

FEATURES
 source Location/Qualifiers
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QY 70 CGGCGTGAGACCT 82
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RESULT 10
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 DEFINITION Sequence 104 from Patent WO0192512.
 ACCESSION AX323966
 VERSION AX323966.1 GI:18094717
 KEYWORDS
 SOURCE Hordeum vulgare
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.

REFERENCE
 AUTHORS Kmiec,E.B., Gamper,H.B., Rice,M.C. and Kim,J.
 TITLE Targeted chromosomal genomic alterations in plants using modified
 single stranded oligonucleotides
 JOURNAL Patent: WO 0192512-A 104 06-DEC-2001;
 UNIVERSITY OF DELAWARE (US)

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RESULT 11
 AX499488/c
 LOCUS AX499488 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 795 from Patent EP1229046.
 ACCESSION AX499488
 VERSION AX499488.1 GI:23381781
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Zhan,J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 795 07-AUG-2002;
 Neomica, Inc. (US)

FEATURES
 source Location/Qualifiers
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ORIGIN
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QY 385 CTGCACCGCGCCG 397
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 AX499489/c
 LOCUS AX499489 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 796 from Patent EP1229046.
 ACCESSION AX499489
 VERSION AX499489.1 GI:23381782
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Zhan,J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 796 07-AUG-2002;
 Neomica, Inc. (US)

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 LOCUS AX499490 17 bp DNA linear PAT 27-SEP-2002
 DEFINITION Sequence 797 from Patent EP1229046.
 ACCESSION AX499490
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 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Zhan,J.
 TITLE Human testis expressed patched like protein
 JOURNAL Patent: EP 1229046-A 797 07-AUG-2002;
 Neomica, Inc. (US)

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ACCESSION AX499491
VERSION AX499491.1 GI:23381784
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Zhan, J.
JOURNAL Human testis expressed patched like protein
Patent: EP 1229046-A 798 07-AUG-2002;
Neomica, Inc. (US)
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ACCESSION AX499492
VERSION AX499492.1 GI:23381785
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Zhan, J.
JOURNAL Human testis expressed patched like protein
Patent: EP 1229046-A 799 07-AUG-2002;
Neomica, Inc. (US)
LOCATION/Qualifiers
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FEATURES
source

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
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Db 13 CTGCACCGCGCCG 1

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LOCUS AX673599 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2044 from Patent WO03004526.

ACCESSION AX673599
VERSION AX673599.1 GI:29331947
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Telerman, A., Anson, R. and Tuijinder, M.
JOURNAL Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
Patent: WO 03004526-A 2044 16-JAN-2003;
Molecular Engines Laboratories (FR)
LOCATION/Qualifiers
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FEATURES
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Db 2 ATCCTTTCACTG 14

RESULT 17
LOCUS AX687581/c 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 313 from Patent EP1281758.
ACCESSION AX687581
VERSION AX687581.1 GI:29410277
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
Patent: EP 1281758-A 313 05-FEB-2003;
Neomica, Inc. (US)
LOCATION/Qualifiers
1. 17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCCG 258
Db 17 CTCCTGAGGCCG 5

RESULT 18
LOCUS AX687582/c 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 314 from Patent EP1281758.
ACCESSION AX687582
VERSION AX687582.1 GI:29410278
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 314 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGAGCCCC 258
16 CTCCTGAGAGCCCC 4
Db
RESULT 19
AX687583 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 315 from Patent EPI281758.
DEFINITION AX687583
ACCESSION AX687583.1 GI:29410279
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 315 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 2.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGAGCCCC 258
15 CTCCTGAGAGCCCC 3
Db
RESULT 20
AX687584 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 316 from Patent EPI281758.
DEFINITION AX687584
ACCESSION AX687584.1 GI:29410280
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 316 05-FEB-2003;
Aeomica, Inc. (US)
JOURNAL

FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGAGCCCC 258
14 CTCCTGAGAGCCCC 2
Db
RESULT 21
AX687585 17 bp DNA linear PAT 31-MAR-2003
LOCUS Sequence 317 from Patent EPI281758.
DEFINITION AX687585
ACCESSION AX687585.1 GI:29410281
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 317 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 2.2%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGAGCCCC 258
13 CTCCTGAGAGCCCC 1
Db
RESULT 22
AX735945 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 1535 from Patent WO03025177.
DEFINITION AX735945
ACCESSION AX735945.1 GI:30515222
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 Telerman, A., Anson, R. and Thijnder, M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments
TITLE Patent: WO 03025177-A 1535 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 242 TCACCTCTCTGAG 254
 |||||
 16 TCACCTCTCTGAG 4

Db 16 TCACCTCTCTGAG 4

RESULT 23
 BD104902 17 bp DNA linear PAT 27-AUG-2002
 LOCUS Kit and method for determining HLA type.
 ACCESSION BD104902
 VERSION BD104902.1 GI:22650476
 KEYWORDS WO 0192572-A/1006.
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Inoko,H., Kagiya,T., Ichihara,T., Matsumura,Y., Moriya,S. and Nishida,M.
 TITLE Kit and method for determining HLA type
 JOURNAL Patent: WO 0192572-A 1006 06-DEC-2001;
 NISSHINO INDUSTRIES INC.,SYSTEM RESEARCH INC.,HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA

COMMENT OS Artificial Sequence
 PN WO 0192572-A/1006
 PD 06-DEC-2001
 PF 01-JUN-2001 WO 2001JP004662
 PR 01-JUN-2000 JP 00P 164798
 PI HIDETOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, PI

FEATURES
 source 1. .17
 Location/Qualifiers
 /organism="Artificial Sequence".
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN
 Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCACGTGG 172
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 3 GGCTGCACGTGG 15

Db 3 GGCTGCACGTGG 15

RESULT 24
 AR241182 19 bp DNA linear PAT 20-DEC-2002
 LOCUS Sequence 9 from patent US 6468983.
 ACCESSION AR241182
 VERSION AR241182.1 GI:27286412
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
 TITLE Nbase V activators and antisense oligonucleotides effective to treat telomerase-expressing malignancies
 JOURNAL Patent: US 6468983-A 9 22-OCT-2002;
 FEATURES Location/Qualifiers

source 1. .19
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 2.2%; Score 13; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGGTGCAAT 407
 |||||
 3 CCGGGGTGCAAT 15

Db 3 CCGGGGTGCAAT 15

RESULT 25
 AR253259 19 bp DNA linear PAT 20-DEC-2002
 LOCUS AR253259/c
 ACCESSION AR253259
 VERSION AR253259.1 GI:27301682
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Short,J.M.
 TITLE Non-stochastic generation of genetic vaccines
 JOURNAL Patent: US 6479258-A 4 12-NOV-2002;
 FEATURES Location/Qualifiers
 source 1. .19
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 2.2%; Score 13; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGTCTCCCA 520
 |||||
 15 GTTCGTCTCCCA 3

Db 15 GTTCGTCTCCCA 3

RESULT 26
 AX129413/c 19 bp DNA linear PAT 15-MAY-2001
 LOCUS AX129413
 DEFINITION Sequence 631 from Patent WO0130362.
 ACCESSION AX129413
 VERSION AX129413.1 GI:14135718
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Robbins,J.W. and Tritz,R.
 TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
 JOURNAL Patent: WO 0130362-A 631 03-MAY-2001;
 IMMUSOL, INC. (US)
 FEATURES Location/Qualifiers
 source 1. .19
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 /note="Cdk6 ribozyme binding site"

ORIGIN
 Query Match 2.2%; Score 13; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 GCCTGGAGAGGC 493

Db 17 GCCTGGGAAGGC 5

RESULT 27
AX129414/c 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 632 from Patent WO0130362.
ACCESSION AX129414
VERSION AX129414.1 GI:14135719
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Robbins,J.M. and Tritz,R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 632 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Cdk6 ribozyme binding site"

ORIGIN
Query Match 2.2%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 481 GCCTGGGAAGGC 493
Db 16 GCCTGGGAAGGC 4

RESULT 28
AX259857/c 19 bp DNA linear PAT 26-OCT-2001
LOCUS AX259857
DEFINITION Sequence 84 from Patent WO0172822.
ACCESSION AX259857
VERSION AX259857.1 GI:16508931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamaillard,M.
TITLE Genes involved in intestinal inflammatory diseases and use thereof
JOURNAL Patent: WO 0172822-A 84 04-OCT-2001;
Fondation Jean Dausset-Ceph (FR)
FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.2%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 TCCGCTGGGCTAA 65
Db 18 TCCGCTGGGCTAA 6

RESULT 29
BD084645 19 bp DNA linear PAT 27-AUG-2002
LOCUS BD084645

DEFINITION
ACCESSION BD084645
VERSION BD084645.1 GI:22630255
KEYWORDS JP 2001524100-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Silverman,R.H., Kondo,S., Cowell,J.K., Li,G. and Torrence,P.F.
TITLE Ribase L activators and antisense oligonucleotides effective to treat telomerase-expressing malignancies.
JOURNAL Patent: JP 2001524100-A 9 27-NOV-2001;
THE CLEVELAND CLINIC FOUNDATION,NATIONAL INSTITUTES OF HEALTH
OS Artificial Sequence
COMMENT PN JP 2001524100-A/9
PD 27-NOV-2001
PF 13-APR-1998 JP 1998546125
PR 21-APR-1997 US 60/044507,03-FEB-1998 US 09/018125 PI
ROBERT H SILVERMAN,SEIJI KONDO,JOHN K COWELL,GUYING LI,PAUL F
PI TORRENCE
PC C07H21/00,C07H21/02,C12Q1/68,A61K48/00
CC Description of Artificial Sequence: oligonucleotide FH Key
FT source 1..19
FT Location/Qualifiers
1..19
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="Genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.2%; Score 13; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 395 CCGGGCTGCAAT 407
Db 3 CCGGGCTGCAAT 15

RESULT 30
DOGp43801 20 bp DNA linear MAM 17-JAN-1996
LOCUS DOGp43801
DEFINITION Dog (Clone: CXK.438) primer for STS 438, 5' end.
ACCESSION L24320
VERSION L24320.1 GI:402023
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 1 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
TITLE One hundred and one new simple sequence repeat-based markers for the canine genome
JOURNAL Mamm. Genome 6 (3), 192-195 (1995)
MEDLINE 95268214
PUBMED 7749226
COMMENT Original source text: Canis familiaris (library: E. Ostrander, in pBluecript+), adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia, Mailstop M318
Seattle, WA 98104, USA
e-mail: EOstrander@hl.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes

PCR Cycles: 33
Final Extension: 74 degrees C for 5.00 minutes.

FEATURES	Location/Qualifiers
source	1. .20

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Primer_bind
ORIGIN
1. .20
/cisue_11b="B. Ostrander, in pbluescript+"

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Query Match      2.2% ; Score 13 ; DB 4 ; Length 20 ;
Best Local Similarity 100.0% ; Pred. No. 2.5e+05 ;
Matches 13 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
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QY	303	CCCCAACCTCAGT	315
Db	1	CCCCAACCTCAGT	13

RESULT 31	LOCUS	SEQUENCE	DEFINITION	ACCSSION	20 bp	DNA	1linear	PAT 14-FEB-2001
AR098868	AR098868	Sequence 3 from patent US 6077685.						

REFERENCE	1 (bases 1 to 20)
AUTHORS	Trofater, J.A., Maccollin, M.M. and Guseila, J.F.
TITLE	Tumor suppressor meelin and antibodies thereof
JOURNAL	Patent: US 6077665-A 3 20-JUN-2000;
FEATURES	Location/Qualifiers
SOURCE	1. 20

Query	March	2.2%	Score	13	DB	6	Length	20	
Best	Local	Similarity	100.0%	Pred. No.	2.5e+05				
Matches	13	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	118	ACATCCCTTTGAC	130						
Db	8	ACATCCCTTTGAC	20						

LOCUS	20 bp	DNA	PAT 10-JUN-1998
LOCUS	179708		
DEFINITION	Sequence 3 from patent US 5707863.		
ACCESSION	U78000		
RESULT 32	179708		

ORIGIN	
Query Match	2.2%; Score 13; DB 6; Length 20;
Best Local Similarity	100.0%; Pred. No. 2.5e+05;

	Matches	13, Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	118	ACATCCTTTTCAC	130						
Db	8	ACATCCTTTTCAC	20						

RESULT 33					
AR257223/c					
LOCUS	AR257223	20 bp	DNA		
DEFINITION	Sequence	78 from patent US 6485974.		linear	PAT 20-DEC-2002
ACCESSION	U0357223				

REFERENCE	1 (bases 1 to 20)
AUTHORS	Popoff, I.
TITLE	Antisense modulation of PPN2 expression
JOURNAL	Patent: US 645974-A 78 26-NOV-2002;
FEATURES	Location/Qualifiers
source	1..20

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Query Match      2.2%  Score 13;  DB 6;  Length 20;
Best Local Similarity 100.0%  Pred. No. 2.5e+05;
Matches 13;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      108  TGACAGCTCTACA 120
      |||||
      13  TGACAGCTCTACA 1

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RESULT 34	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AR337175	AR337175	Sequence 100 from patent US 6566135.	20 bp	DNA	linear	PAT 17-AUG-2003	
				AR337175			
				AR337175.1	GI:33723029		
					Unknown.		
					Unknown.		

REFERENCE	1 (bases 1 to 20)
AUTHORS	Watt,A.T.
TITLE	Antisense modulation of caspase 6 expression
JOURNAL	Patent: US 6566135-A 100 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..20

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QY      447 TACTTTTGTAGAA 455
         |||||
Db      4 TACTTTTGTAGAA 16

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RESULT	35
AX428287/c	
LOCUS	AX428287
DEFINITION	Sequence from Patent WO0233056.
ACCESSION	AX428287
VERSION	AX428287.1
KEYWORDS	GI:21538245
SOURCE	Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1 Koehler, R.H.
Regulation of human serine-threonine protein kinase
JOURNAL
Patent: WO 0233056-A 9 25-APR-2002;

FEATURES

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="PCR primer"

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 194 TCTCGACTGGGA 206
|||||
19 TCTCGACTGGGA 7

Db 19 TCTCGACTGGGA 7

RESULT 36
BD138115/c 20 bp DNA linear PAT 18-SEP-2002

LOCUS BD138115
DEFINITION Antisense modulation of human MDM2 expression.

ACCESSION BD138115
VERSION BD138115.1 GI:22333060

KEYWORDS JP 2002508944-A/41.

SOURCE unclassified

ORGANISM unclassified

REFERENCE 1 (bases 1 to 20)
Mizuguchi, L.J., Nepo, P., Graham, M.J., Montia, B.P. and Cowser, L.M.

TITLE Antisense modulation of human MDM2 expression
JOURNAL Patent: JP 2002508944-A 41 26-MAR-2002;

COMMENT OS Unidentified
IS PHARMACEUTICALS INC

PI LOREN J MIRAGLIA, PAMELA NERO, MARK J GRAHAM, BRETT P MONIA, LEX M

PC C12N15/09, A61K48/00, A61P9/10, A61P17/06, A61P35/00, C07H21/04//

PC C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

CC Antisense modulation of human MDM2 expression FH Key

Location/Qualifiers

FT source 1..20

Location/Qualifiers

1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.2%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCGAGGCGC 376
|||||

Db 19 GAGCCGAGGCGC 7

RESULT 37

AX358112/c 13 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 7 from Patent WO0194394.

ACCESSION AX358112
VERSION AX358112.1 GI:18674859

SOURCE

Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Jilka, J.M., Hood, E.E. and Howard, J.A.
Novel plant promoter sequences and methods of use for same
Patent: WO 0194394-A 7 13-DEC-2001;

FEATURES

Location/Qualifiers
1..13
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 TGCCACGTGGA 174
|||||

Db 13 TGCCACGTGGA 2

RESULT 38
I43304/c 14 bp DNA linear PAT 07-OCT-1997

LOCUS I43304
DEFINITION Sequence 122 from patent US 5631146.

ACCESSION I43304
VERSION I43304.1 GI:2468548

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 14)
Szoestak, J.W. and Huijenga, D.E.

TITLE DNA aptamers and catalysts that bind adenosine or
adenosine-5'-phosphates and methods for isolation thereof
JOURNAL Patent: US 5631146-A 122 20-MAY-1997;

Location/Qualifiers

1..14
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 180 CTTCCTCCGCTA 191
|||||

Db 13 CTTCCTCCGCTA 2

RESULT 39

A09427/c 15 bp DNA linear PAT 09-NOV-1993

LOCUS A09427
DEFINITION Oligonucleotide (b3).

ACCESSION A09427
VERSION A09427.1 GI:490532

KEYWORDS

synthetic construct
synthetic construct
artificial sequences.


```

REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S. and Yamada,H.
TITLE Process for production of somatostatin
JOURNAL Patent: EP 0197558-A 33 15-OCT-1986;
          FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
  source
    1.15
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4

RESULT 40
LOCUS A10630 15 bp DNA linear PAT 02-DEC-1993
DEFINITION Oligonucleotide (B3).
ACCESSION A10630
VERSION A10630.1 GI:490758
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S., Ono,H. and Kitaguchi,T.
TITLE Process for production of gamma-interferon
JOURNAL Patent: EP 0176916-A 15 09-APR-1986;
          FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
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    1.15
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
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Query Match      2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4

RESULT 41
LOCUS A11578 15 bp DNA linear PAT 16-NOV-1993
DEFINITION oligonucleotide 'b3'.
ACCESSION A11578
VERSION A11578.1 GI:491120
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S., Ono,H. and Kitaguchi,T.
TITLE 59 Valine insulin-like growth factor I and process for production thereof
JOURNAL Patent: EP 0156893-A 74 23-OCT-1985;
          FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
  source
    1.15
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

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ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4

RESULT 42
LOCUS A24554 15 bp DNA linear PAT 24-JAN-1995
DEFINITION PROM38 PCR primer.
ACCESSION A24554
VERSION A24554.1 GI:833371
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS DNA, DNA CONSTRUCTS, CELLS AND PLANTS DERIVED THEREFROM
TITLE Patent: WO 9307275-A 5 15-APR-1993;
JOURNAL Location/Qualifiers
FEATURES
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    1.15
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257
Db 3 CTCCTGAGGCC 14

RESULT 43
LOCUS A35098 15 bp DNA linear PAT 06-DEC-1996
DEFINITION Synthetic IGF-I gene oligo.
ACCESSION A35098
VERSION A35098.1 GI:1926757
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ueda,I., Niwa,M., Saitoh,Y., Saitoh,S. and Kuwamoto,C.
TITLE Process for production of insulin-like growth factor I and plasmid for production thereof
JOURNAL Patent: EP 0219814-A 48 29-APR-1987;
          FUJISAWA PHARMACEUTICAL CO., LTD
FEATURES
  source
    1.15
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    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
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Query Match      2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 TCCGCTACATCT 196
Db 15 TCCGCTACATCT 4

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	ORIGIN
Query Match	2.0%; Score 12; DB 6; length 15;
Best Local Similarity	100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	246 CTCCTGGAGCCC 257
Db	3 CTCCTGGAGCCC 14
RESULT 46	
A68725	
LOCUS	A68725 15 bp DNA
DEFINITION	Sequence 9 from Patent WO980175.
ACCESSION	A68725
VERSION	A68725.1 GI:4759720
KEYWORDS	.
SOURCE	unidentified
ORGANISM	unidentified

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RESULT 48
AR091792
LOCUS AR091792 15 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 35 from patent US 5994519.
ACCESSION AR091792
VERSION AR091792.1 GI:10018546
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Osbourn,J,Kaharine., Derbyshire,E.Joy., McCafferty,J.Gerald.,
Vaughan,T.John. and Johnson,K.Stuart.
TITLE Labelling and selection of molecules
FEATURES
location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"

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ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 49

AR126265 15 bp DNA PAT 16-MAY-2001
LOCUS Sequence 35 from patent US 6180336.
DEFINITION AR126265
ACCESSION AR126265
VERSION AR126265.1 GI:14112858
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Osbourn, J. Katharine., Derbyshire, F. Joy., McCafferty, J. Gerald.,
Vaughan, T. John, and Johnson, K. Stuart.
TITLE Labelling and selection of molecules
JOURNAL Patent: US 6180336-A 35 30-JAN-2001;
FEATURES Location/Qualifiers
1. 15
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 50 15 bp DNA PAT 06-FEB-1997
LOCUS 128574
DEFINITION Sequence 27 from patent US 5571937.
ACCESSION 128574
VERSION 128574.1 GI:1819350
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Watanabe, K. A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 27 05-NOV-1996;
FEATURES Location/Qualifiers
1. 15
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTCCTC 186
Db 13 TTGCTCTCTCCTC 2

RESULT 51 15 bp DNA PAT 07-OCT-1997
LOCUS 158736

DEFINITION Sequence 27 from patent US 5652350.

ACCESSION 158736
VERSION 158736.1 GI:2477974
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Watanabe, K. A., Ren, W.-Y. and Weil, R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 27 29-JUL-1997;
FEATURES Location/Qualifiers
1. 15
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTCTCCTC 186
Db 13 TTGCTCTCTCCTC 2

RESULT 52 15 bp DNA PAT 10-JUN-1998
LOCUS 181235
DEFINITION Sequence 10 from patent US 5710026.
ACCESSION 181235
VERSION 181235.1 GI:3209525
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Sprecher, C. A.
TITLE Cytoplasmic antiprotease-2 and cytoplasmic antiprotease-3 and
JOURNAL coding sequences
PATENT: US 5710026-A 10 20-JAN-1998;
FEATURES Location/Qualifiers
1. 15
source

ORIGIN /organism="unknown"
/mol_type="unassigned DNA"

Query Match 2.0%; Score 12; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
Db 3 CTCCTGGAGCCC 14

RESULT 53 15 bp DNA PAT 10-JUN-1998
LOCUS 182215
DEFINITION Sequence 10 from patent US 5712117.
ACCESSION 182215
VERSION 182215.1 GI:3210512
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 15)
AUTHORS Sprecher, C. A.
TITLE Cytoplasmic antiprotease-2 and coding sequences
JOURNAL Patent: US 5712117-A 10 27-JAN-1998;
FEATURES Location/Qualifiers
1. 15
source

ORIGIN /mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14

RESULT 54
ARI84255 15 bp DNA linear PAT 20-APR-2002
LOCUS
DEFINITION Sequence 35 from patent US 6342588.
ACCESSION ARI84255
VERSION ARI84255.1 GI:20228224
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Unclassified.
1 (bases 1 to 15)
Osborn,J.Katharine., Derbyshire,E.Joy., McCafferty,J.Gerald.,
Vaughan,T.John. and Johnson,K.Stuart.
Labelling and selection of molecules
Patent: US 6342588-A 35 29-JAN-2002;
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14

RESULT 55
AR258241 15 bp DNA linear PAT 20-DEC-2002
LOCUS
DEFINITION AR258241
ACCESSION AR258241
VERSION AR258241.1 GI:27308418
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

Unclassified.
1 (bases 1 to 15)
Osborn,J.K., Derbyshire,E.J., McCafferty,J.G., Vaughan,T.J. and
Johnson,K.S.
Labelling and selection of molecules
Patent: US 6489123-A 35 03-DEC-2002;
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14

RESULT 56

BD096388 15 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Novel scavenger receptor.
ACCESSION BD096388
VERSION BD096388.1 GI:22641976
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

synthetic construct
artificial sequences.
1 (bases 1 to 15)
Wakamiya,N.
Novel scavenger receptor
Patent: WO 0159107-A 18 16-AUG-2001;
FUSO PHARMACEUTICAL INDUSTRIES LTD,NOBUTAKA WAKAMIYA
OS Artificial Sequence
PN WO 0159107-A/18
PD 16-AUG-2001
PF 08-FEB-2001 WO 2001JP000874
PR 14-FEB-2000 JP 00P 35155,10-OCT-2000 JP 00P 309068 PI
NOBUTAKA WAKAMIYA
PC C12N15/12,C07K14/47,C12N1/21,C12N5/10,C12P21/02,C07K16/28, PC
C12P21/08,
PC A01K67/027,A61K45/06,A61P9/10,A61P3/06,A61P3/10 CC Sequence
of a lambda gti15' Sequencing Primer. FH Key
Location/Qualifiers
FT source 1. .15
/organism="Artificial Sequence".
Location/Qualifiers
1. .15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 12; DB 6; Length 15;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14

RESULT 57
E07495/c 16 bp DNA linear PAT 29-SEP-1997
LOCUS
DEFINITION Synthetic DNA for probe.
ACCESSION E07495
VERSION E07495.1 GI:2175633
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

unidentified
unclassified.
1 (bases 1 to 16)
Yamanishi,K., Yamamoto,T. and Mori,H.
ANALYSIS OF HUMAN HERPES VIRUS 6 TYPE @ (3754/24) HHV-6) DNA AND
DISCRIMINATION OF SUB-TYPE
Patent: JP 1994133799-A 4 17-MAY-1994;
INTERNATL REAGENTS CORP
OS None
OS Artificial sequences.
PN JP 1994133799-A/4
PD 17-MAY-1994
PF 27-OCT-1992 JP 1992311416
PI YAMANISHI KOICHI, YAMAMOTO TARESHI, MORI HIROYUKI PC
C12Q1/68,C12Q1/68,C12N15/11,C12N15/38;
CC strandness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1. .16

FEATURES FT /organism='Artificial sequences'.
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 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 2.0%; Score 12; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 CATGAAATCA 507
 DB 12 CATGAAATCA 1

RESULT 58
 LOCUS AR361170 16 bp DNA PAT 17-AUG-2003
 DEFINITION Sequence 41 from patent US 6599700.
 ACCESSION AR361170
 VERSION AR361170.1 GI:33768875
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE 1 (bases 1 to 16)
 AUTHORS Bellacosa, A.
 TITLE Methods for detection of transition single-nucleotide polymorphisms
 JOURNAL Patent: US 6599700-A 41 29-JUL-2003;
 FEATURES Location/Qualifiers
 1.16
 /organism="unknown"
 /mol_type="genomic DNA"

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Query Match 2.0%; Score 12; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 CTACATCCTTT 127
 DB 15 CTACATCCTTT 4

RESULT 59
 LOCUS AR040435 17 bp DNA PAT 29-SEP-1999
 DEFINITION Sequence 1283 from patent US 5807743.
 ACCESSION AR040435
 VERSION AR040435.1 GI:5959798
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Stinchcomb, D.T. and McSwiggen, J.A.
 TITLE Interleukin-2 receptor gamma-chain ribozymes
 JOURNAL Patent: US 5807743-A 1283 15-SEP-1998;
 FEATURES Location/Qualifiers
 1.17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 CCGAGGCCCT 259
 DB 13 CCGAGGCCCT 2

RESULT 60
 LOCUS BD241420 17 bp DNA PAT 17-JUL-2003
 DEFINITION Methods and products related to genotyping and DNA analysis.
 ACCESSION BD241420
 VERSION BD241420.1 GI:33051190
 KEYWORDS JP 2002525127-A/367.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 17)
 AUTHORS Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.
 TITLE Methods and products related to genotyping and DNA analysis
 JOURNAL Patent: JP 2002525127-A 367 13-AUG-2002;
 MASSACHUSETTS INSTITUTE OF TECHNOLOGY

COMMENT OS Homo sapiens (human)
 PN JP 2002525127-A/367
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
 CC Methods and products related to genotyping and DNA analysis FH
 Key Location/Qualifiers
 FT source 1.17
 /organism="Homo sapiens (human)".
 FT Location/Qualifiers
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

FEATURES source
 1.17
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 409 GCCATCATGACC 420
 DB 5 GCCATCATGACC 16

RESULT 61
 LOCUS I26836 17 bp DNA PAT 07-OCT-1996
 DEFINITION Sequence 59 from patent US 5561041.
 ACCESSION I26836
 VERSION I26836.1 GI:1606706
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Sidransky, D.
 TITLE Nucleic acid mutation detection by analysis of sputum
 JOURNAL Patent: US 5561041-A 59 01-OCT-1996;
 FEATURES Location/Qualifiers
 1.17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGGCTGCATGAA 501
 DB 13 GGGCTGCATGAA 501

Db 5 GGCGCTGCATGAA 16

RESULT 62

LOCUS 127966 17 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 138 from patent US 5567809.
 ACCESSION 127966
 VERSION 127966.1 GI:1818742
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 138 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGAGC 255
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 1 ACCTCCTGAGC 12

Db 1 ACCTCCTGAGC 12

RESULT 63

LOCUS 127987 17 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 159 from patent US 5567809.
 ACCESSION 127987
 VERSION 127987.1 GI:1818763
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 159 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGAGC 255
 |||||
 1 ACCTCCTGAGC 12

Db 1 ACCTCCTGAGC 12

RESULT 64

LOCUS 191577 17 bp DNA linear PAT 01-DEC-1998
 DEFINITION Sequence 59 from patent US 5726019.
 ACCESSION 191577
 VERSION 191577.1 GI:3936047
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Sidransky,D.

TITLE Analysis of sputum by amplification and detection of mutant nucleic acid sequences

JOURNAL Patent: US 5726019-A 59 10-MAR-1998;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 490 GGCGCTGCATGAA 501
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 5 GGCGCTGCATGAA 16

Db 5 GGCGCTGCATGAA 16

RESULT 65

LOCUS AX214609/c 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 51 from Patent WO0159103.
 ACCESSION AX214609
 VERSION AX214609.1 GI:15524652
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 51 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers
 source 1..17
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
 |||||
 17 CTGAGCCCGAGG 6

Db 17 CTGAGCCCGAGG 6

RESULT 66

LOCUS AX215505/c 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 947 from Patent WO0159103.
 ACCESSION AX215505
 VERSION AX215505.1 GI:15525548
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Blatt,L., McSwiggen,J. and Chowrira,B.M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 947 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
 McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned RNA"

ORIGIN /db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 12 CTGAGCCCGAGG 1

RESULT 67
LOCUS AX216404/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 1846 from Patent WO0159103.
ACCESSION AX216404
VERSION AX216404.1 GI:15526465
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., Mswiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
PATENT: WO 0159103-A 1846 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Mswiggen, James (US); Chowrira, Bharat M. (US)

JOURNAL

FEATURES
source 1.17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 14 CTGAGCCCGAGG 3

RESULT 68
LOCUS AX216978/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2420 from Patent WO0159103.
ACCESSION AX216978
VERSION AX216978.1 GI:15527039
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., Mswiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
PATENT: WO 0159103-A 2420 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Mswiggen, James (US); Chowrira, Bharat M. (US)

JOURNAL

FEATURES
source 1.17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 16 CTGAGCCCGAGG 5

RESULT 69
LOCUS AX216979/c 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2421 from Patent WO0159103.
ACCESSION AX216979
VERSION AX216979.1 GI:15527040
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., Mswiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
PATENT: WO 0159103-A 2421 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
Mswiggen, James (US); Chowrira, Bharat M. (US)

JOURNAL

FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
Db 15 CTGAGCCCGAGG 4

RESULT 70
LOCUS AX262772 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 163 from Patent WO0173002.
ACCESSION AX262772
VERSION AX262772.1 GI:16511571
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
PATENT: WO 0173002-A 163 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)

JOURNAL

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 71
AX262773/c
LOCUS AX262773 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 164 from Patent WO0173002.
ACCESSION AX262773
VERSION AX262773.1 GI:16511572
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kmiec, E.B., Gampel, H.B. and Rice, M.C.
AUTHORS Targeted chromosomal genomic alterations with modified single
TITLE stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 164 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
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QY 16 ATGAACCGGAGG 27
Db 15 ATGAACCGGAGG 4
RESULT 72
AX262800
LOCUS AX262800 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 191 from Patent WO0173002.
ACCESSION AX262800
VERSION AX262800.1 GI:16511599
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kmiec, E.B., Gampel, H.B. and Rice, M.C.
AUTHORS Targeted chromosomal genomic alterations with modified single
TITLE stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 191 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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QY 16 ATGAACCGGAGG 27
Db 2 ATGAACCGGAGG 13
RESULT 73
AX262801/c
LOCUS AX262801 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 192 from Patent WO0173002.
ACCESSION AX262801

VERSION AX262801.1 GI:16511600
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Kmiec, E.B., Gampel, H.B. and Rice, M.C.
AUTHORS Targeted chromosomal genomic alterations with modified single
TITLE stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 192 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
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QY 16 ATGAACCGGAGG 27
Db 16 ATGAACCGGAGG 5
RESULT 74
AX460261/c
LOCUS AX460261 17 bp DNA linear PAT 08-JUL-2002
DEFINITION Sequence 114 from Patent WO0244736.
ACCESSION AX460261
VERSION AX460261.1 GI:21725885
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1 Tazi-Ahmini, R., Bavik, C., Ward, S., Duff, G. and Cork, M.
AUTHORS Diagnosis and treatment of disease
TITLE Patent: WO 0244736-A 114 06-JUN-2002;
JOURNAL Molecular Skincare Limited (GB)
FEATURES
source Location/Qualifiers
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/organism="synthetic construct"
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/note="Primer"
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QY 192 CATCTCGAGCTG 203
Db 17 CATCTCGAGCTG 6
RESULT 75
AX499487/c
LOCUS AX499487 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 794 from Patent EP1259046.
ACCESSION AX499487
VERSION AX499487.1 GI:23381780
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhan, J.

TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 794 07-AUG-2002;
Aeomica, Inc. (US)
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ORIGIN

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QY 386 TGCACCGCGCGC 397
DB 17 TGCACCGCGCGC 6

RESULT 76
AX499493/c 17 bp DNA linear PAT 27-SEP-2002
LOCUS AX499493
DEFINITION Sequence 800 from Patent EP1229046.
ACCESSION AX499493
VERSION AX499493.1 GI:23381786
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 800 07-AUG-2002;
Aeomica, Inc. (US)
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QY 385 CTGCACCGCGCC 396
DB 12 CTGCACCGCGCC 1

RESULT 77
AX4545291 17 bp DNA linear PAT 26-NOV-2002
LOCUS AX4545291
DEFINITION Sequence 804 from Patent EP1243660.
ACCESSION AX4545291
VERSION AX4545291.1 GI:25810502
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 804 25-SEP-2002;
Aeomica, Inc. (US)
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QY 165 CCACGTGAATT 176
DB 6 CCACGTGAATT 17

RESULT 78
AX545292 17 bp DNA linear PAT 26-NOV-2002
LOCUS AX545292
DEFINITION Sequence 805 from Patent EP1243660.
ACCESSION AX545292
VERSION AX545292.1 GI:25810503
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 805 25-SEP-2002;
Aeomica, Inc. (US)
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QY 165 CCACGTGAATT 176
DB 5 CCACGTGAATT 16

RESULT 79
AX545293 17 bp DNA linear PAT 26-NOV-2002
LOCUS AX545293
DEFINITION Sequence 806 from Patent EP1243660.
ACCESSION AX545293
VERSION AX545293.1 GI:25810504
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 806 25-SEP-2002;
Aeomica, Inc. (US)
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QY 165 CCACGTGAATT 176
DB 4 CCACGTGAATT 15

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RESULT 80
LOCUS AX545294 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 807 from Patent EP1243660.
ACCESSION AX545294
VERSION AX545294.1 GI:25810505
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Zhang, J., Gu, Y. and Nguyen, C.T.
AUTHORS Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 807 25-SEP-2002;
Aeomica, Inc. (US)
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QY 165 CCACGTGAATT 176
Db 3 CCACGTGAATT 14

RESULT 81
LOCUS AX545295 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 808 from Patent EP1243660.
ACCESSION AX545295
VERSION AX545295.1 GI:25810506
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Zhang, J., Gu, Y. and Nguyen, C.T.
AUTHORS Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 808 25-SEP-2002;
Aeomica, Inc. (US)
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QY 165 CCACGTGAATT 176
Db 2 CCACGTGAATT 13

RESULT 82
LOCUS AX545296 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 809 from Patent EP1243660.
ACCESSION AX545296
VERSION AX545296.1 GI:25810507
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
REFERENCE Zhang, J., Gu, Y. and Nguyen, C.T.
AUTHORS Human udp-galnac:polypeptide n-acetylglucosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 809 25-SEP-2002;
Aeomica, Inc. (US)
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 CCACGTGAATT 176
Db 1 CCACGTGAATT 12

RESULT 83
LOCUS AX673640 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 2085 from Patent WO03004526.
ACCESSION AX673640
VERSION AX673640.1 GI:29331988
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Telerman, A., Anson, R. and Tadjinder, M.
AUTHORS Sequences involved in phenomena of tumour suppression, tumour
TITLE reversion, apoptosis and/or resistance to viruses and their use as
JOURNAL Patent: WO 03004526-A 2085 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
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QY 355 CGCAGGCTGAG 366
Db 4 CGCAGGCTGAG 15

RESULT 84
LOCUS AX687580 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 312 from Patent EP1281758.
ACCESSION AX687580
VERSION AX687580.1 GI:29410276
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
TITLE mdz12

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JOURNAL Patent: EP 1281758-A 312 05-FEB-2003;
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGAGAGCCCC 258
Db 17 TCCTGAGAGCCCC 6

RESULT 85
LOCUS AX687586 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 318 from Patent EP1281758.
ACCESSION AX687586
VERSION AX687586.1 GI:29410282
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Shannon,M., Gu,Y. and Nguyen,C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
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  Patent: EP 1281758-A 318 05-FEB-2003;
  Aeomica, Inc. (US)
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QY 246 CTCCTGAGAGCCC 257
Db 12 CTCCTGAGAGCCC 1

RESULT 86
LOCUS AX688061 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 793 from Patent EP1281758.
ACCESSION AX688061
VERSION AX688061.1 GI:29410759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Shannon,M., Gu,Y. and Nguyen,C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
  Patent: EP 1281758-A 793 05-FEB-2003;
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QY 434 TTTACTGCTGGA 445
Db 6 TTTACTGCTGGA 17

RESULT 87
LOCUS AX688062 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 794 from Patent EP1281758.
ACCESSION AX688062
VERSION AX688062.1 GI:29410760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Shannon,M., Gu,Y. and Nguyen,C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
  Patent: EP 1281758-A 794 05-FEB-2003;
  Aeomica, Inc. (US)
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QY 434 TTTACTGCTGGA 445
Db 5 TTTACTGCTGGA 16

RESULT 88
LOCUS AX688063 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 795 from Patent EP1281758.
ACCESSION AX688063
VERSION AX688063.1 GI:29410761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1 Shannon,M., Gu,Y. and Nguyen,C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
  Patent: EP 1281758-A 795 05-FEB-2003;
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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445

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REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 4429 05-FEB-2003;
Aeomica, Inc. (US)
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QY 365 AGCCCGAGGGGC 376
DB 16 AGCCCGAGGGGC 5
RESULT 94
AX691698 17 bp DNA linear PAT 31-MAR-2003
LOCUS AX691698
DEFINITION Sequence 4430 from Patent EP1281758.
ACCESSION AX691698
VERSION AX691698.1 GI:29414636
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 4430 05-FEB-2003;
JOURNAL Aeomica, Inc. (US)
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QY 365 AGCCCGAGGGGC 376
DB 15 AGCCCGAGGGGC 4
RESULT 95
AX691699 17 bp DNA linear PAT 31-MAR-2003
LOCUS AX691699
DEFINITION Sequence 4431 from Patent EP1281758.
ACCESSION AX691699
VERSION AX691699.1 GI:29414637
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 4431 05-FEB-2003;
JOURNAL Aeomica, Inc. (US)

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 365 AGCCCGAGGGGC 376
DB 14 AGCCCGAGGGGC 3
RESULT 96
AX691700 17 bp DNA linear PAT 31-MAR-2003
LOCUS AX691700
DEFINITION Sequence 4432 from Patent EP1281758.
ACCESSION AX691700
VERSION AX691700.1 GI:29414638
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 4432 05-FEB-2003;
JOURNAL Aeomica, Inc. (US)
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DB 13 AGCCCGAGGGGC 2
RESULT 97
AX691701 17 bp DNA linear PAT 31-MAR-2003
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ACCESSION AX691701
VERSION AX691701.1 GI:29414639
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 Shannon, M., Gu, Y. and Nguyen, C.T.
AUTHORS Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
TITLE Patent: EP 1281758-A 4433 05-FEB-2003;
JOURNAL Aeomica, Inc. (US)
FEATURES
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1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match 2.0%; Score 12; DB 6; Length 17;
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376
DB 12 AGCCCGAGGGGC 1

RESULT 98
AX724214 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1901 from Patent WO03025176.
ACCESSION AX724214
VERSION AX724214.1 GI:30503557
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijthof, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1901 27-MAR-2003;
Molecular Engines Laboratories (FR)
LOCATION/Qualifiers
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

FEATURES
source

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 TGAGACCTACCT 86
DB 5 TGAGACCTACCT 16

RESULT 99
AX724376 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2063 from Patent WO03025176.
ACCESSION AX724376
VERSION AX724376.1 GI:30503719
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijthof, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2063 27-MAR-2003;
Molecular Engines Laboratories (FR)
LOCATION/Qualifiers
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

FEATURES
source

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 457 GAAACCATGAA 468

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ACCATGAAGA 472
DB 5 ACCATGAAGA 16

RESULT 100
AX724877 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2564 from Patent WO03025176.
ACCESSION AX724877
VERSION AX724877.1 GI:30504220
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijthof, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 2564 27-MAR-2003;
Molecular Engines Laboratories (FR)
LOCATION/Qualifiers
1. .17
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/mol_type="unassigned DNA"
/db_xref="taxon:10090"

FEATURES
source

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGACCTTGCT 141
DB 6 CTGACCTTGCT 17

RESULT 101
AX728700 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 334 from Patent WO03025175.
ACCESSION AX728700
VERSION AX728700.1 GI:30508043
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijthof, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025175-A 334 27-MAR-2003;
Molecular Engines Laboratories (FR)
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ACCATGAAGA 472
DB 5 ACCATGAAGA 16

RESULT 102

LOCUS	AX730426	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 2060 from Patent WO03025175.				
ACCESSION	AX730426				
VERSION	AX730426.1 GI:30509769				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1. Telerman, A., Amsen, R., and Tuijinder, M.				
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines				
JOURNAL	Patent: WO 03025175-A 2060 27-MAR-2003;				
FEATURES	Molecular Engines Laboratories (FR)				
source	Location/Qualifiers				
	1..17				
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	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	313 AGCTGAGATC 324				
DB	12 AGCTGAGATC 1				
RESULT 103					
LOCUS	AX731908	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 3542 from Patent WO03025175.				
ACCESSION	AX731908				
VERSION	AX731908.1 GI:30511251				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1. Telerman, A., Amsen, R., and Tuijinder, M.				
TITLE	Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines				
JOURNAL	Patent: WO 03025175-A 3542 27-MAR-2003;				
FEATURES	Molecular Engines Laboratories (FR)				
source	Location/Qualifiers				
	1..17				
	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	355 CGAAGGCTGAG 366				
DB	4 CGAAGGCTGAG 15				
RESULT 104					
LOCUS	AX734602	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 192 from Patent WO03025177.				
ACCESSION	AX734602				
VERSION	AX734602.1 GI:30513879				

KEYWORDS	ORGANISM	REFERENCE	JOURNAL	FEATURES	ORIGIN
KEYWORDS	Homo sapiens (human)	1 Telerman, A., Amson, R. and Tuijinder, M. Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or resistance to viruses and the use thereof as medicaments Patent: WO 03025177-A 192 27-MAR-2003; Molecular Engines Laboratories (FR)	JOURNAL	location/Qualifiers	source
SOURCE				1. 17 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
SOURCE					
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Gaps 0;				
LOCUS	AX734928	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 518 from Patent WO03025177.				
ACCESSION	AX734928				
VERSION	AX734928.1				
KEYWORDS	GI:30514205				
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE					
JOURNAL					
FEATURES					
SOURCE					
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Gaps 0;				
LOCUS	AX736368	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 1958 from Patent WO03025177.				
ACCESSION	AX736368				
VERSION	AX736368.1				
KEYWORDS	GI:30515645				
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE					
JOURNAL					
FEATURES					
SOURCE					
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Gaps 0;				
LOCUS	AX736368	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 1958 from Patent WO03025177.				
ACCESSION	AX736368				
VERSION	AX736368.1				
KEYWORDS	GI:30515645				
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE					
JOURNAL					
FEATURES					
SOURCE					
ORIGIN					
Query Match	2.0%; Score 12; DB 6; Length 17;				
Best Local Similarity	100.0%; Pred. No. 9.1e+05;				
Matches	12; Conservative 0; Mismatches 0; Gaps 0;				
LOCUS	AX736368	17 bp	DNA	linear	PAT 08-MAY-2003
DEFINITION	Sequence 1958 from Patent WO03025177.				
ACCESSION	AX736368				
VERSION	AX736368.1				
KEYWORDS	GI:30515645				
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE					
JOURNAL					
FEATURES					
SOURCE					
ORIGIN	</				

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REFERENCE
1
AUTHORS
1
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL
Patent: WO 03025177-A 1958 27-MAR-2003;
Molecular Engines Laboratories (FR)
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1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match
2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
354 CCGCAGGCTGA 365
|||||
14 CCGCAGGCTGA 3

RESULT 107
LOCUS
AX739569
DEFINITION
Sequence 5159 from Patent WO03025177.
ACCESSION
AX739569
VERSION
AX739569.1 GI:30518866
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS
Telerman,A., Amson,R. and Tuijnder,M.
TITLE
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL
Patent: WO 03025177-A 5159 27-MAR-2003;
Molecular Engines Laboratories (FR)
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/mol_type="unassigned DNA"
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2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
355 CCGCAGGCTGAG 366
|||||
4 CCGCAGGCTGAG 15

RESULT 108
LOCUS
AX757736
DEFINITION
Sequence 1057 from Patent WO03040369.
ACCESSION
AX757736
VERSION
AX757736.1 GI:32252352
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS
Telerman,A., Amson,R. and Tuijnder,M.
TITLE
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines

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JOURNAL
Patent: WO 03040369-A 1057 15-MAY-2003;
Molecular Engines Laboratories (FR)
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1.17
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/mol_type="unassigned DNA"
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2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
500 AAAATTCAGTTC 511
|||||
17 AAAATTCAGTTC 6

RESULT 109
LOCUS
AX760197
DEFINITION
Sequence 3518 from Patent WO03040369.
ACCESSION
AX760197
VERSION
AX760197.1 GI:32254813
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS
Telerman,A., Amson,R. and Tuijnder,M.
TITLE
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL
Patent: WO 03040369-A 3518 15-MAY-2003;
Molecular Engines Laboratories (FR)
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1.17
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
355 CCGCAGGCTGAG 366
|||||
4 CCGCAGGCTGAG 15

RESULT 110
LOCUS
AX762288
DEFINITION
Sequence 5609 from Patent WO03040369.
ACCESSION
AX762288
VERSION
AX762288.1 GI:32256904
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1
AUTHORS
Telerman,A., Amson,R. and Tuijnder,M.
TITLE
Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL
Patent: WO 03040369-A 5609 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1.17
/organism="Homo sapiens"

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ORIGIN /mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGAGCTGAG 366
|||||
DB 4 CGCAGAGCTGAG 15

RESULT 111
BD198764 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD198764/c
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD198764
VERSION BD198764.1 GI:33008534
KEYWORDS JP 2002509721-A/1790.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
AUTHORS 1 (bases 1 to 17)
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL Method and reagent for treating diseases or conditions concerning
PATENT: JP 2002509721-A 1790 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/1790
PD 02-APR-2002 JP 2000541291
PR 24-MAR-1999 JP 2000541291
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1.17
FT /organism="Homo sapiens (human)".
Location/Qualifiers
1.17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTGGAGCCCTG 260
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DB 12 CTGGAGCCCTG 1

RESULT 112
BD200907 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD200907
DEFINITION molecule participating in vasculogenic response.
ACCESSION BD200907
VERSION BD200907.1 GI:33010677
KEYWORDS JP 2002509721-A/3933.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 17)
JOURNAL Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
PATENT: JP 2002509721-A 3933 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/3933
PD 02-APR-2002 JP 2000541291
PR 24-MAR-1999 JP 2000541291
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1.17
FT /organism="Homo sapiens (human)".
Location/Qualifiers
1.17
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/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 TTTACCAATTCA 46
|||||
DB 6 TTTACCAATTCA 17

RESULT 113
A24633 18 bp DNA linear PAT 02-OCT-1995
LOCUS A24633
DEFINITION SYNTHETIC ECORI primer.
ACCESSION A24633
VERSION A24633.1 GI:1248003
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Zabeau,M. and Vos,P.
TITLE Selective restriction fragment amplification : a general method for
JOURNAL DNA fingerprinting
PATENT: EP 0534858-A 43 31-MAR-1993;
KEYGENE N.V.
Location/Qualifiers
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 TTTACCAATTCA 47
|||||

Db 6 TTACCAATTCOA 17

RESULT 114
AR076773

LOCUS AR076773 18 bp DNA linear PAT 30-AUG-2000

DEFINITION Sequence 17 from patent US 5959097.

ACCESSION AR076773

VERSION AR076773.1 GI:10003519

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Monta, B.P. and Cowsett, L.M.
Antisense modulation of MEK2 expression
Patent: US 5959097-A 17 28-SEP-1999;
Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGACTTTGGT 141
|||||
6 CTGACTTTGGT 17

Db

RESULT 115
AR085592

LOCUS AR085592 18 bp DNA linear PAT 01-SEP-2000

DEFINITION Sequence 28 from patent US 5981732.

ACCESSION AR085592

VERSION AR085592.1 GI:10012359

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Cowsett, L.M.
Antisense modulation of G-alpha-13 expression
Patent: US 5981732-A 28 09-NOV-1999;
Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGAATCTTCAC 330
|||||
7 AGAATCTTCAC 18

Db

RESULT 116
AR092798

LOCUS AR092798 18 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 13 from patent US 5998206.

ACCESSION AR092798

VERSION AR092798.1 GI:10019550

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Cowsett, L.M.

AUTHORS

TITLE Antisense inhibition of human G-alpha-12 expression

JOURNAL Patent: US 5998206-A 13 07-DEC-1999;
Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGAATCTTCAC 330
|||||
3 AGAATCTTCAC 14

Db

RESULT 117
AR096294

LOCUS AR096294 18 bp DNA linear PAT 08-SEP-2000

DEFINITION Sequence 15 from patent US 6007231.

ACCESSION AR096294

VERSION AR096294.1 GI:10024973

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
Vajj, J. and Bishop, R.
Method of computer aided automated diagnostic DNA test design, and
apparatus therefor
Patent: US 6007231-A 15 28-DEC-1999;
Location/Qualifiers
1. 18
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
3 TCGTCTCTCCAG 14

Db

RESULT 118
BD260529

LOCUS BD260529 18 bp DNA linear PAT 17-JUL-2003

DEFINITION Polymorphic loci that differentiate Escherichia coli O157:H7 from
other strains.

ACCESSION BD260529

VERSION BD260529.1 GI:33070299

KEYWORDS JP 2002531130-A/8.
synthetic construct
artificial sequences.

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 18)
Tarr, P.I.
Polymorphic loci that differentiate Escherichia coli O157:H7 from
other strains
Patent: JP 2002531130-A 8 24-SEP-2002;
CHILDREN'S HOSPITAL AND REGIONAL MEDICAL CENTER
OS Artificial Sequence
PN JP 2002531130-A/8
PD 24-SEP-2002
PP 08-DEC-1999 JP 2000586917
PR 08-DEC-1999 US 60/111493
PT PHILIP I TARR
PC C12N15/09, C12N15/09, C07K16/12, C12N1/15, C12N1/19, C12N1/21 PC
C12N5/10, C12N9/04,
PC

JOURNAL

COMMENT

C1201/68,G01N33/53,G01N33/566,G01N33/577// PC
 C12221/08,
 PC (C12N9/04,C12R1:19),(C12Q1/68,C12R1:19),C12N15/00,C12N5/00, PC
 C12N15/00
 CC primer
 FH Key
 FT source
 Location/Qualifiers
 1.18
 /organism="Artificial Sequence",
 /mol_type="synthetic construct"
 /db_xref="taxon:32630"

FEATURES

source

Query Match
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

186 CCGCTACATCTC 197
 |||||
 4 CCGCTACATCTC 15

Db

RESULT 119

127949

LOCUS 127949 18 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 12: from patent US 5567809.
 ACCESSION 127949
 VERSION 127949.1 GI:1818725

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 121 22-OCT-1996;
 FEATURES
 source
 1.18
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

244 ACCTCCTGGAGC 255
 |||||
 2 ACCTCCTGGAGC 13

Db

RESULT 120

127986/c

LOCUS 127986 18 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 158 from patent US 5567809.
 ACCESSION 127986
 VERSION 127986.1 GI:1818762

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 158 22-OCT-1996;
 FEATURES
 source
 1.18
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

244 ACCTCCTGGAGC 255
 |||||
 17 ACCTCCTGGAGC 6

Db

RESULT 121

AR361496

LOCUS AR361496 18 bp DNA PAT 17-AUG-2003
 DEFINITION Sequence 17 from patent US 6599728.
 ACCESSION AR361496
 VERSION AR361496.1 GI:33769344

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Morin,G.B., Funk,W.D. and Piatyzek,M.A.
 TITLE Second mammalian tankyrase
 JOURNAL Patent: US 6599728-A 17 29-JUL-2003;
 FEATURES
 source
 1.18
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

246 CTCCTGGAGCCC 257
 |||||
 3 CTCCTGGAGCCC 14

Db

RESULT 122

AX05650

LOCUS AX05650 18 bp DNA PAT 13-JAN-2001
 DEFINITION Sequence 8 from Patent WO0073499.
 ACCESSION AX05650
 VERSION AX05650.1 GI:12228790

KEYWORDS

Kluyveromyces marxianus

Kluyveromyces marxianus

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

REFERENCE 1
 Smith,T., Maher,M., Martin,C., Janes,G., Rossau,R. and van der

AUTHORS

Weide,M.

Nucleic acid probes and methods for detecting clinically important

fungal pathogens

Patent: WO 0073499-A 8 07-DEC-2000;

INNOGENETICS N.V. (BE) ; Enterprise Ireland (trading as Bioresearch

Ireland) (IE)

FEATURES

source

1.18
 /organism="Kluyveromyces marxianus"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4911"

ORIGIN

Query Match
 Best Local Similarity 100.0%; Score 12; DB 6; Length 18;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

510 TCGTCTCCAG 521
 |||||
 6 TCGTCTCCAG 17

Db

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RESULT 123
AX391661/c
LOCUS AX391661 18 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 42 from Patent EP1184468.
ACCESSION AX391661
VERSION AX391661.1 GI:15700267
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Yamamoto,N.C., Okamoto,T.C. and Suzuki,T.C.
METHOD for sequencing using probe arrays
Patent: EP 1184468-A 42 06-MAR-2002;
JOURNAL CANON KABUSHIKI KAISHA (JP)
FEATURES
source
location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:13630"
/note="sample oligonucleotide"
ORIGIN

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Query Match Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 16 ATGAACCGGAGG 27
    |||||
Db 18 ATGAACCGGAGG 7

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RESULTS	124				
AX391684					
LOCUS	AX391684	18 bp	DNA		
DEFINITION	Sequence 65 from Patent EP1184468.				
ACCESSION	AX391684			linear	
VERSION	AX391684.1				PAT 23-MAR-2002
KEYWORDS					
SOURCE	unidentified				
ORGANISM	unidentified				
	unclassified.				
REFERENCE	1				
AUTHORS	Yamamoto,N.C., Okamoto,T.C. and Suzuki,T.C.				
TITLE	Method for sequencing using probe arrays				
JOURNAL	Patent: EP 1184468-A 65 06-MAR-2002;				
	CANON KABUSHIKI KAISHA (JP)				
FEATURES	Location/Qualifiers				
source	1..18				

Query Match	2.0%	Score 12	DB 6	length 18
Best Local Similarity	100.0%	Pred. No. 9.1e+05		
Matches 12	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	16 ATGAACCGGAGG 27			
Db	1 ATGAACCGGAGG 12			
RESULT 125				
AX391810/C				
LOCUS	AX391810	18 bp	DNA	linear
DEFINITION	Sequence 42 from Patent Ep1184467.			
ACCESSION	AX391810			
VERSION	AX391810.1	GI:19700394		
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			

REFERENCE
1
artificial sequences.

AUTHORS
Yamamoto, N., Okamoto, T., Tanaka, S. and Suzuki, T

TITLE
Screening method for gene variation

JOURNAL
Patent: EP 1184467-A 42 06-MAR-2002;
CANON KABUSHIKI KAISHA (JP)

FEATURES
location/Qualifiers
1..18
/object="artificial construct"

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/organism="synthetic construct
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Sample oligonucleotide"

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Query Match      2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	126				
AX391833					
LOCUS	AX391833	18 bp	DNA	linear	PAT 23-MAR-2002
DEFINITION	Sequence 65 from Patent EP184467.				
ACCESSION	AX391833				
VERSION	AX391833.1	GI:19700417			
KEYWORDS					

SOURCE	ORGANISM	unidentified
REFERENCE	1	unclassified.
AUTHORS	Yamamoto, N., Okamoto, T., Tanaka, S. and Suzuki, T	
TITLE	Screening method for gene variation	
JOURNAL	Patent : EP 1184467-A 65 06-MR-2002; CANON KABUSHIKI KAISHA (JP)	
FEATURES	Location/Qualifiers	
SOURCE	1. 18	

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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="p53 fragment oligonucleotide"

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Query Match      2.0%; Score 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Gaps 0;
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QY	16	ATGAACCGGAGG	27
Db	1	ATGAACCGGAGG	12

RESULT 127				
AX398505	AX398505	18 bp	DNA	linear
LOCUS	Sequence 1 from Patent EP1188475.			
DEFINITION	AX398505			
ACCESSION	AX398505.1	GI:21261206		
VERSION				
KEYWORDS				
SOURCE	synthetic construct			
ORGANISM	synthetic construct			
	artificial bequences.			

```
REFERENCE
1. Okamoto, T., Yamamoto, N., Watanabe, H. and Suzuki, T.
  Method for making probe support and apparatus used for the method
  Patent: JP 1189475-A 1 20-MAR-2002;
  CANON KABUSHIKI KAISHA (JP)
  Location/Qualifiers
FEATURES
source
1. .18
  /organism="synthetic construct"
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ORIGIN

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Base Oligonucleotide for preparation of a probe"

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
|||||
1 ATGAACCGAGG 12

RESULT 128
AX453818/c 18 bp DNA linear PAT 06-JUL-2002

LOCUS AX453818
DEFINITION Sequence 42 from Patent EP1213361.
ACCESSION AX453818
VERSION AX453818.1 GI:21713487
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Okamoto, T., Yamamoto, N. and Suzuki, T.
TITLE Terminal labeled probe array and method of making it
JOURNAL Patent: EP 1213361-A 42 12-JUN-2002;
CANON KABUSHIKI KAISHA (JP)
LOCATION/Qualifiers

FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthesized"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
|||||
18 ATGAACCGAGG 7

RESULT 129
AX453841 18 bp DNA linear PAT 06-JUL-2002

LOCUS AX453841
DEFINITION Sequence 65 from Patent EP1213361.
ACCESSION AX453841
VERSION AX453841.1 GI:21713510
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Okamoto, T., Yamamoto, N. and Suzuki, T.
TITLE Terminal labeled probe array and method of making it
JOURNAL Patent: EP 1213361-A 65 12-JUN-2002;
CANON KABUSHIKI KAISHA (JP)
LOCATION/Qualifiers

FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthesized"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
|||||
1 ATGAACCGAGG 12

RESULT 130
AX587524 18 bp DNA linear PAT 10-JAN-2003

LOCUS AX587524
DEFINITION Sequence 34 from Patent WO0236751.
ACCESSION AX587524
VERSION AX587524.1 GI:27656340
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Wernet, P.
TITLE Human cord blood derived unrestricted somatic stem cells (ussc)
JOURNAL Patent: WO 0236751-A 34 10-MAY-2002;
Kourion Therapeutics GmbH (DE)
LOCATION/Qualifiers

FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3 primer for the beta actin gene"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGATCTTCA 328
|||||
6 TGAGATCTTCA 17

RESULT 131
BD000011 18 bp DNA linear PAT 31-JAN-2002

LOCUS BD000011
DEFINITION Probe-coupling substrate, process for producing the same,
probe-array, method for detecting target substance, method for
specifying base sequence of single-stranded nucleic acid in
sample, and method for quantitating the target substance in the
sample.

ACCESSION BD000011
VERSION BD000011.1 GI:18623090
KEYWORDS JP 2000270896-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto, H., Yamamoto, N. and Suzuki, T.
TITLE Probe-coupling substrate, process for producing the same,
probe-array, method for detecting target substance, method for
specifying base sequence of single-stranded nucleic acid in sample,
and method for quantitating the target substance in the sample
Patent: JP 2000270896-A 1 03-OCT-2000;
CANON INC AVTEN PHARMACEUT CO LTD
OS Artificial Sequence
PN JP 2000270896-A/1
PD 03-OCT-2000
PT 28-JAN-1999 JP 1999019915

COMMENT
JOURNAL
PI HIASHI OKAMOTO, NOBUKO YAMAMOTO, TOMOHIRO SUZUKI PC
CI201/68, CI2M1/00, CI2N15/09, GO1N33/566, CI2N15/00 CC
FH Key
FT source 1.18
/organism="Artificial Sequence".
/mol_type="genomic DNA"

FEATURES
source 1.18
/organism="synthetic construct"
/mol_type="genomic DNA"

ORIGIN /db_xref="taxon:32630"

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 12

Db

RESULT 132
 BD000053/c
 LOCUS
 DEFINITION BD000053 18 bp DNA linear PAT 31-JAN-2002
 Probe-coupling substrate, process for producing the same,
 specifying base sequence of single-stranded nucleic acid in
 sample, and method for quantitating the target substance in the
 sample.

ACCESSION BD000053 GI:18623132
 VERSION JP 2000270896-A/43.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Okamoto,H., Yamamoto,N. and Suzuki,T.
 TITLE Probe-coupling substrate, process for producing the same,
 probe-array, method for detecting target substance, method for
 specifying base sequence of single-stranded nucleic acid in
 sample, and method for quantitating the target substance in the sample
 Patent: JP 2000270896-A 43 03-OCT-2000;

JOURNAL CANON INC ANTEN PHARMACEUT CO LTD
 OS Artificial Sequence
 PN JP 2000270896-A/43
 PD 03-OCT-2000
 PF 28-JAN-1999 JP 1999019915
 PR

COMMENT

ORIGIN

FEATURES
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 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 7

Db

RESULT 133
 BD010932
 LOCUS
 DEFINITION BD010932 18 bp DNA linear PAT 31-JAN-2002
 Selective restriction fragment amplification: general DNA
 fingerprint method Selective restriction fragment amplification:
 general DNA fingerprint method.

ACCESSION BD010932 GI:18639305
 VERSION JP 2001061486-A/42.
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 18)

AUTHORS Szabo,M. and Foss,P.
 TITLE Selective restriction fragment amplification: general DNA
 fingerprint method
 JOURNAL Patent: JP 2001061486-A 42 13-MAR-2001;
 COMMENT KEYGENE NV
 OS Artificial Sequence
 PN JP 2001061486-A/42
 PD 13-MAR-2001
 PF 25-JUL-2000 JP 2000224187
 PR 24-SEP-1991 GB 91402542.4
 PI MARK SZABO,PIETER FOSS
 PC C12N15/09,C12Q1/68,C12N15/00
 CC
 FH
 FT

FEATURES
 source
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 7

Db

RESULT 134
 BD133664/c
 LOCUS
 DEFINITION BD133664 18 bp DNA linear PAT 18-SEP-2002
 Method for screening mutated gene.

ACCESSION BD133664
 VERSION BD133664.1 GI:23228609
 KEYWORDS JP 2002071687-A/42.
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Tanaka,S.
 TITLE Method for screening mutated gene
 JOURNAL Patent: JP 2002071687-A 42 12-MAR-2002;
 CANON INC
 OS Artificial Sequence
 PN JP 2002071687-A/42
 PD 12-MAR-2002
 PF 31-AUG-2000 JP 2000263396
 PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,SHINYA TANAKA
 PC G01N33/53,C12M1/00,C12N15/09,C12Q1/68,G01N33/566,PC
 G01N37/00,
 CC C12N15/00
 FH Sample oligonucleotide
 FT key
 FT source
 1. .18
 /organism="Artificial Sequence".

FEATURES
 source
 1. .18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 7

Db

```

RESULT 135
BD135697/c 18 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
  BD135697 Method for detecting subjective component in specimen sample, and
  substrate for detection used therefor.
ACCESSION
  BD135697 GI:23230642
VERSION
  JP 2002065274-A/1.
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
ORGANISM
  artificial sequences.
  1 (bases 1 to 18)
REFERENCE
  Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.
  Method for detecting subjective component in specimen sample, and
  substrate for detection used therefor
  Patent: JP 2002065274-A 1 05-MAR-2002;
JOURNAL
  CANON INC
COMMENT
  OS Artificial Sequence
  PN JP 2002065274-A/1
  PD 05-MAR-2002
  PF 31-AUG-2000 JP 200263395
  PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI AKIRA SHIMIZU
  PC C12N15/09,C12M1/00,C12M1/40,C12Q1/68,G01N31/22,G01N33/53, PC
  G01N33/566,
  PC G01N35/02,G01N35/10,G01N37/00,C12N15/00,G01N35/06 CC DNA
  probe for hybridizing with gene encoding p53 FH Key
  Location/Qualifiers
  FT source 1..18
  /organism='Artificial Sequence'.
  Location/Qualifiers
  1..18
  /organism='synthetic construct'
  /mol_type='genomic DNA'
  /db_xref='taxon:32630'

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
Db 18 ATGACCGGAGG 7

RESULT 136
BD135742/c 18 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION
  BD135742 Method for detecting subjective component in specimen sample, and
  substrate for detection used therefor.
ACCESSION
  BD135742 GI:23230687
VERSION
  JP 2002065274-A/46.
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
ORGANISM
  artificial sequences.
  1 (bases 1 to 18)
REFERENCE
  Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.
  Method for detecting subjective component in specimen sample, and
  substrate for detection used therefor
  Patent: JP 2002065274-A 46 05-MAR-2002;
JOURNAL
  CANON INC
COMMENT
  OS Artificial Sequence
  PN JP 2002065274-A/46
  PD 05-MAR-2002
  PF 31-AUG-2000 JP 200263395
  PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI AKIRA SHIMIZU
  PC C12N15/09,C12M1/00,C12M1/40,C12Q1/68,G01N31/22,G01N33/53, PC
  G01N33/566,
  PC G01N35/02,G01N35/10,G01N37/00,C12N15/00,G01N35/06 CC DNA
  probe for hybridizing with gene encoding
  mutated p53;named

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CC as probe 42
in Table 1
Key Location/Qualifiers
FH source 1..18
FT /organism='Artificial Sequence'.
FT Location/Qualifiers

FEATURES
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  1..18
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  /mol_type='genomic DNA'
  /db_xref='taxon:32630'

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
Db 18 ATGACCGGAGG 7

RESULT 137
BD161008/c 18 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION
  BD161008 Terminal-labeled probe-array and method for preparing it, and
  method for evaluating target mass using the same.
ACCESSION
  BD161008 GI:27866766
VERSION
  JP 2002153284-A/42.
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
ORGANISM
  artificial sequences.
  1 (bases 1 to 18)
REFERENCE
  Okamoto,T., Yamamoto,N. and Suzuki,T.
  Terminal-labeled probe-array and method for preparing it, and
  method for evaluating target mass using the same
  Patent: JP 2002153284-A 42 28-MAY-2002;
JOURNAL
  CANON INC
COMMENT
  OS Artificial Sequence
  PN JP 2002153284-A/42
  PD 28-MAY-2002
  PF 24-NOV-2000 JP 2000357446
  PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
  C12N15/09,C12Q1/68,G01N31/22,G01N33/53,G01N37/00, PC
  C12N15/00
  CC Description of Artificial Sequence:Synthesized FH Key
  Location/Qualifiers
  FT source 1..18
  /organism='Artificial Sequence'.
  Location/Qualifiers
  1..18
  /organism='synthetic construct'
  /mol_type='genomic DNA'
  /db_xref='taxon:32630'

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
Db 18 ATGACCGGAGG 7

RESULT 138
BD161031 18 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION
  BD161031 Terminal-labeled probe-array and method for preparing it, and
  method for evaluating target mass using the same.
ACCESSION
  BD161031 GI:27866789
VERSION
  JP 2002153284-A/65.
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto,T., Yamamoto,N. and Suzuki,T.
TITLE Terminal-labeled probe-array and method for preparing it, and method for evaluating target mass using the same
JOURNAL Patent: JP 2002153284-A 65 28-MAY-2002;
CANON INC

COMMENT OS Artificial Sequence
PN JP 2002153284-A/65
PD 28-MAY-2002
PF 24-NOV-2000 JP 2000357446
PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12Q1/68,G01N31/22,G01N33/53,G01N33/566,G01N37/00, PC
C12N15/00
CC Description of Artificial Sequence:Synthesized FH Key
Location/Qualifiers
FT source 1. .18
/organism='Artificial Sequence'.
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

RESULT 139
BD162058/c
LOCUS 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for detecting nucleic acid.
ACCESSION BD162058
VERSION BD162058.1 GI:27867816
KEYWORDS JP 2002176999-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Suzuki,T.
TITLE Method for detecting nucleic acid
JOURNAL Patent: JP 2002176999-A 1 25-JUN-2002;
CANON INC

COMMENT OS Artificial Sequence
PN JP 2002176999-A/1
PD 25-JUN-2002
PF 12-DEC-2000 JP 2000377349
PI TOMOHIRO SUZUKI
PC C12Q1/68,C07H21/04,C12N15/09,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
CC Target gene fragment for probe hybridization FH Key
Location/Qualifiers
FT source 1. .18
/organism='Artificial Sequence'.
Location/Qualifiers
1. .18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 7

Db

RESULT 140
BD162059
LOCUS 18 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for detecting nucleic acid.
ACCESSION BD162059
VERSION BD162059.1 GI:27867817
KEYWORDS JP 2002176999-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Suzuki,T.
TITLE Method for detecting nucleic acid
JOURNAL Patent: JP 2002176999-A 2 25-JUN-2002;
CANON INC

COMMENT OS Artificial Sequence
PN JP 2002176999-A/2
PD 25-JUN-2002 JP 2000377349
PF 12-DEC-2000 JP 2000377349
PI TOMOHIRO SUZUKI
PC C12Q1/68,C07H21/04,C12N15/09,G01N33/53,G01N33/566,G01N33/58,
PC C12N15/00
CC hybridization probe
FH Key
Location/Qualifiers
FT source 1. .18
/organism='Artificial Sequence'.
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

RESULT 141
BD167503/c
LOCUS 18 bp DNA linear PAT 17-JAN-2003
DEFINITION A method of analyzing a base sequence of a nucleic acid.
ACCESSION BD167503
VERSION BD167503.1 GI:27873315
KEYWORDS WO 0233068-A/42.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T. and Suzuki,T.
TITLE A method of analyzing a base sequence of a nucleic acid
JOURNAL Patent: WO 0233068-A 42 25-APR-2002;
CANON KK,NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI

COMMENT OS Artificial Sequence
PN WO 0233068-A/42
PD 25-APR-2002
PF 18-OCT-2000 WO 2000JP007244
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12Q1/68,G01N33/566,G01N33/53
CC Sample oligonucleotide
FH Key
Location/Qualifiers
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
1 ATGACCGGAGG 12

Db

source 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 7

Db

RESULT 142
BD174790 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION liquid discharge device for production of probe carrier, device for
production of probe carrier using the liquid discharge device, and
process for producing the probe carrier.
BD174790
BD174790.1 GI:29120482
KEYWORDS JP 2002257694-A/1
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaneko, M. and Watanabe, H.
TITLE liquid discharge device for production of probe carrier, device for
production of probe carrier using the liquid discharge device, and
process for producing the probe carrier
Patent: JP 2002257694-A 1 11-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002257694-A/1
PD 11-SEP-2002
PF 28-FEB-2001 JP 2001055970
PI MINO KANEKO, HIDEORI WATANABE
PC G01N15/00, B41J2/05, C12M1/00, C12N15/09, G01N33/53, G01N33/566, PC
G01N35/10
PC G01N37/00, B41J3/04, C12N15/00, G01N35/06
CC Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1..18
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 12

Db

RESULT 143
BD174965 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION Process for producing probe carrier using liquid discharge device
and device used for this process.
BD174965
BD174965.1 GI:29120659
KEYWORDS JP 2002257836-A/1
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto, T.
TITLE Process for producing probe carrier using liquid discharge device
and device used for this process
Patent: JP 2002257836-A 1 11-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002257836-A/1
PD 11-SEP-2002
PF 28-FEB-2001 JP 2001055971
PI TADASHI OKAMOTO
PC G01N35/10, B41J2/01, B41J2/04, C12M1/00, C12N15/09, G01N37/00, PC
G01N35/06
PC B41J3/04, B41J3/04, C12N15/00
CC Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1..18
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 12

Db

RESULT 144
BD175058 18 bp DNA linear PAT 18-MAR-2003
LOCUS
DEFINITION A method of preparing a probe array.
BD175058
BD175058.1 GI:29120752
KEYWORDS JP 2002253251-A/1
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaneko, M. and Watanabe, H.
TITLE A method of preparing a probe array
Patent: JP 2002253251-A 1 10-SEP-2002;
JOURNAL CANON INC

COMMENT OS Artificial Sequence
PN JP 2002253251-A/1
PD 10-SEP-2002
PF 28-FEB-2001 JP 2001055972
PI MINO KANEKO, HIDEORI WATANABE
PC C12N15/09, C12M1/00, G01N33/53, G01N33/566, G01N37/00, C12N15/00 CC
Base Oligonucleotide for preparation of a probe FH Key
LOCATION/Qualifiers
FT source 1..18
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
|||||
18 ATGACCGGAGG 12

Db

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RESULT 145
BD176986/c 18 bp DNA linear PAT 16-APR-2003
LOCUS BD176986
DEFINITION Method of analyzing nucleic acid base sequence.
ACCESSION BD176986
VERSION BD176986.1 GI:30014245
KEYWORDS JP 2002306166-A/42.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,H. and Suzuki,T.
TITLES Method of analyzing nucleic acid base sequence
JOURNAL Patent: JP 2002306166-A 42 22-OCT-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002306166-A/42
PD 22-OCT-2002
PE 31-AUG-2000 JP 2000263506
PI NOBUKO YAMAMOTO,HISASHI OKAMOTO,TOMOHIRO SUZUKI PC
C12N15/09,C12O1/68//C12M1/00,C12N15/00
CC Sample originucleotide
FH Key Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGACCGGAGG 27
Db 18 ATGACCGGAGG 7
RESULT 146
BD177274 18 bp DNA linear PAT 16-APR-2003
LOCUS BD177274
DEFINITION A method of preparing a probe array and a device used therefor.
ACCESSION BD177274
VERSION BD177274.1 GI:30014535
KEYWORDS JP 2002318232-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Watanabe,H., Okamoto,T., Yamamoto,N. and Suzuki,T.
TITLES A method of preparing a probe array and a device used therefor
JOURNAL Patent: JP 2002318232-A 1 31-OCT-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002318232-A/1
PD 31-OCT-2002
PE 18-SEP-2001 JP 2001283190
PI HIDENORI WATANABE,TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
G01N33/53,G01N37/00//C12M1/00,C12N15/09,C12N15/00 CC Base
Oligonucleotide for preparation of a probe FH Key
Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
1..18
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/mol_type="genomic DNA"

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ORIGIN /db_xref="taxon:32630"
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGACCGGAGG 27
Db 1 ATGACCGGAGG 12
RESULT 147
BD187511 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD187511
DEFINITION Probe carrier, Method and Apparatus for producing probe carrier.
ACCESSION BD187511
VERSION BD187511.1 GI:32997250
KEYWORDS JP 2003014773-A/1.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLES Probe carrier, Method and Apparatus for producing probe carrier
JOURNAL Patent: JP 2003014773-A 1 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/1
PD 15-JAN-2003
PE 28-MAR-2002 JP 2002993024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC
Oligonucleotide to be hybridized with the designed CC
oligonucleotide
CC 'gattgagccctccgttcatt'
FH Key Location/Qualifiers
FT source 1..18
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGACCGGAGG 27
Db 1 ATGACCGGAGG 12
RESULT 148
BD187512 18 bp DNA linear PAT 17-JUL-2003
LOCUS BD187512
DEFINITION Probe carrier, Method and Apparatus for producing probe carrier.
ACCESSION BD187512
VERSION BD187512.1 GI:32997251
KEYWORDS JP 2003014773-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamura,N., Okamoto,T. and Kameyama,M.
TITLES Probe carrier, Method and Apparatus for producing probe carrier
JOURNAL Patent: JP 2003014773-A 2 15-JAN-2003;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2003014773-A/2
PD 15-JAN-2003
PE 28-MAR-2002 JP 2002993024
PI nobuyuki okamura,tadashi okamoto,makoto kameyama CC
Oligonucleotide used as a probe

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to be stabilized on a
CC carrier
Location/Qualifiers.

FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGAGG 27
18 ATGACCGAGG 7

RESULT 149

LOCUS A57967 19 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 33 from Patent EP0743364.
ACCESSION A57967
VERSION A57967.1 GI:3713737
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Narwa,R. and Roques,P.
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding
fragments and their application as reactives for risk evaluation of
HIV-1 mother-foetal transmission

JOURNAL Patent: EP 0743364-A 33 20-NOV-1996;
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)
FEATURES Other publication FR 2734281 961122.
source Location/Qualifiers

1.19

/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186
4 TTGCTCTTCCTC 15

RESULT 150

LOCUS A57968 19 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 34 from Patent EP0743364.
ACCESSION A57968
VERSION A57968.1 GI:3713738
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Narwa,R. and Roques,P.
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding
fragments and their application as reactives for risk evaluation of
HIV-1 mother-foetal transmission

JOURNAL Patent: EP 0743364-A 34 20-NOV-1996;
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)
FEATURES Other publication FR 2734281 961122.
source Location/Qualifiers

1.19

/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186
4 TTGCTCTTCCTC 15

RESULT 151

LOCUS A57969 19 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 35 from Patent EP0743364.
ACCESSION A57969
VERSION A57969.1 GI:3713739
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1
AUTHORS Narwa,R. and Roques,P.
TITLE Nucleic acid fragments derived from the HIV-1 genome, corresponding
fragments and their application as reactives for risk evaluation of
HIV-1 mother-foetal transmission

JOURNAL Patent: EP 0743364-A 35 20-NOV-1996;
COMMENT COMMISSARIAT ENERGIE ATOMIQUE (FR)
FEATURES Other publication FR 2734281 961122.
source Location/Qualifiers

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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186
3 TTGCTCTTCCTC 14

RESULT 152

LOCUS A91527 19 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 54 from Patent WO9824928.
ACCESSION A91527
VERSION A91527.1 GI:6740482
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 19)
AUTHORS Pallisgaard,N. and Hokland,P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 54 11-JUN-1996;
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
location/Qualifiers

FEATURES

source
1.19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 TTCTGCGAGCGA 301
 DB 17 TTCTGCGAGCGA 6

RESULT 153
 LOCUS AR299567/c 19 bp DNA linear PAT 12-JUN-2003
 DEFINITION Sequence 11302 from patent US 6537751.
 ACCESSION AR299567
 VERSION AR299567.1 GI:31686851
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
 TITLE Biallelic markers for use in constructing a high density
 disequilibrium map of the human genome
 JOURNAL Patent: US 6537751-A 11302 25-MAR-2003;
 FEATURES Location/Qualifiers
 source 1..19
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTCC 187
 DB 15 TGCTCTTCTCC 4

RESULT 154
 LOCUS AX023306 19 bp DNA linear PAT 15-SEP-2000
 DEFINITION Sequence 14 from Patent WO015788.
 ACCESSION AX023306
 VERSION AX023306.1 GI:10183718
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Moroz,C.
 TITLE Dna sequence encoding oncofetal ferritin protein
 JOURNAL Patent: WO 0015788-A 14 23-MAR-2000;
 MOROZ CHAYA (II); GARDINO INVESTMENT N V (NL)
 FEATURES Location/Qualifiers
 source 1..19
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257
 DB 7 CTCCTGAGGCC 18

RESULT 155
 LOCUS AX093498 19 bp DNA linear PAT 30-MAR-2001
 DEFINITION Sequence 28 from Patent WO0118198.
 ACCESSION AX093498

VERSION AX093498.1 GI:13509937
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Weissenbach,J. and Hazan,J.
 TITLE Cloning, expression and characterisation of the spg4 gene
 responsible for the most frequent form of autosomal spastic
 paraplegia
 JOURNAL Patent: WO 0118198-A 28 15-MAR-2001;
 CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
 FEATURES Location/Qualifiers
 source 1..19
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Amorce"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATACCTT 452
 DB 1 CTGGAATACCTT 12

RESULT 156
 LOCUS AX247496 19 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 7 from Patent WO0164923.
 ACCESSION AX247496
 VERSION AX247496.1 GI:15862165
 KEYWORDS
 SOURCE Agrobacterium tumefaciens (Rhizobium radiobacter)
 ORGANISM Agrobacterium tumefaciens
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 REFERENCE 1
 AUTHORS Dumas,F., van Gelder,P., Duckely,M., Hohn,B. and Pelczar,P.
 TITLE Vire2-mediated trans-membrane delivery systems
 JOURNAL Patent: WO 0164923-A 7 07-SEP-2001;
 Novartis Research Foundation (CH); Universitaet Basel (CH)
 FEATURES Location/Qualifiers
 source 1..19
 /organism="Agrobacterium tumefaciens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:358"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTGATGACCGG 24
 DB 3 TTGATGACCGG 14

RESULT 157
 LOCUS AX287545 19 bp DNA linear PAT 21-NOV-2001
 DEFINITION Sequence 8 from Patent WO0168853.
 ACCESSION AX287545
 VERSION AX287545.1 GI:117049315
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Roden,R. and Neore,H.

TITLE Immunogenic ovarian cancer genes
JOURNAL Patent: WO 0168853-A 8 20-SEP-2001;
The Johns Hopkins University School of Medicine (US)
FEATURES
source
1. .19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Primer"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 317 TGAGATCTTCA 328
|||||
Db 8 TGAGATCTTCA 19
RESULT 158
AX763549 19 bp DNA linear PAT 25-JUN-2003
LOCUS AX763549
DEFINITION Sequence 62 from Patent WO03040366.
ACCESSION AX763549
VERSION AX763549.1 GI:32257984
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and
Dautry, F.
TITLE Inhibitor oligonucleotides and their use for specific repression of
a gene
JOURNAL Patent: WO 03040366-A 62 15-MAY-2003;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
1. .19
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1. .19
/note="sequence issue du gene p53 humain sauvage"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGAACCGAGG 27
|||||
Db 3 ATGAACCGAGG 14
RESULT 159
AX763550 19 bp DNA linear PAT 25-JUN-2003
LOCUS AX763550
DEFINITION Sequence 63 from Patent WO03040366.
ACCESSION AX763550
VERSION AX763550.1 GI:32257985
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and
Dautry, F.
TITLE Inhibitor oligonucleotides and their use for specific repression of
a gene
JOURNAL Patent: WO 03040366-A 63 15-MAY-2003;

FEATURES
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
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/mol_type="unassigned DNA"
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misc_feature 1. .19
/note="sequence issue du gene p53 humain sauvage"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGAACCGAGG 27
|||||
Db 3 ATGAACCGAGG 14
RESULT 160
AX763551 19 bp DNA linear PAT 25-JUN-2003
LOCUS AX763551
DEFINITION Sequence 64 from Patent WO03040366.
ACCESSION AX763551
VERSION AX763551.1 GI:32257986
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Harel-Bellan, A., Ait-Si, S., Cabon-Georget, F., Chauchereau, A. and
Dautry, F.
TITLE Inhibitor oligonucleotides and their use for specific repression of
a gene
JOURNAL Patent: WO 03040366-A 64 15-MAY-2003;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR)
FEATURES
source
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misc_feature 1. .19
/note="sequence issue du gene p53 humain sauvage"
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Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGAACCGAGG 27
|||||
Db 3 ATGAACCGAGG 14
RESULT 161
AX822525 19 bp DNA linear PAT 11-DEC-2003
LOCUS AX822525/c
DEFINITION Sequence 417 from Patent EP1340818.
ACCESSION AX822525
VERSION AX822525.1 GI:39749153
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
proliferative disorder
JOURNAL Patent: EP 1340818-A 417 03-SEP-2003;
Epigenomics AG (DE)
FEATURES
Location/Qualifiers

source 1.19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection primer for CDH1"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312
12 AACCCCAACCTC 1

Db

RESULT 162
AX826165/c
LOCUS AX826165 19 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 417 from Patent WO03072821.
ACCESSION AX826165
VERSION AX826165.1 GI:39751679
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Adorjan, P., Burger, M., Maier, S., Nimmrich, I., Becker, E., Lesche, R.,
Rujan, T. and Schmitt, A.
TITLE Method and nucleic acids for the analysis of a colon cell
JOURNAL proliferative disorder
Patent: WO 03072821-A 417 04-SBP-2003;
FEATURES
source
1.19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Detection primer for CDH1"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312
12 AACCCCAACCTC 1

Db

RESULT 163
BD023309/c
LOCUS BD023309 19 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for detecting abnormality in chromosome.
ACCESSION BD023309
VERSION BD023309.1 GI:22564532
KEYWORDS JP 2001505428-A/54.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mammalia, Eutheria, Primates, Catarrhini, Homiidae, Homo.
TITLE 1 (bases 1 to 19)
JOURNAL Parigard, N. and Hokurano, P.
Patent: JP 2001505428-A 54 24-APR-2001;
COMMENT
NEILS PARIGARD
PN JP 2001505428-A/54
PD 24-APR-2001
PF 08-DEC-1997 JP 1998525090
PI NEILS PARIGARD, PATER HOKURANO
PC C12N15/09, C12N1/68, G01N33/50, C12N15/00
CC Strandedness: Single;
Topology: Linear;

CC /desc = 'DNA (synthetic)'
FH Key Location/Qualifiers
source 1.19
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 TTCTGCGAGGGA 301
17 TTCTGCGAGGGA 6

Db

RESULT 164
A82447/c
LOCUS A82447 20 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 35 from Patent WO9854360.
ACCESSION A82447
VERSION A82447.1 GI:6732195
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Plasow, G.S. and Wales, R.
TITLE METHODS FOR ANALYZING ANIMAL PRODUCTS
JOURNAL Patent: WO 9854360-A 35 03-DEC-1998;
FEATURES
source
1.20
Location/Qualifiers
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 CACCTCCTGGAG 254
20 CACCTCCTGGAG 9

Db

RESULT 165
AR085567
LOCUS AR085567 20 bp DNA linear PAT 01-SBP-2000
DEFINITION Sequence 3 from patent US 5981732.
ACCESSION AR085567
VERSION AR085567.1 GI:10012334
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
AUTHORS Cowsett, L.M.
TITLE Antisense modulation of G-alpha-13 expression
JOURNAL Patent: US 5981732-A 3 09-NOV-1999;
FEATURES
source
1.20
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
 |||||
 Db 9 AGGATCTTCACC 20

RESULT 166
 LOCUS AR097384 20 bp DNA PAT 14-FEB-2001
 DEFINITION Sequence 8 from patent US 6071726.
 ACCESSION AR097384
 VERSION AR097384.1 GI:12806114
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.
 TITLE Method, reagents and kit for diagnosis and targeted screening for
 p53 mutations
 JOURNAL Patent: US 6071726-A 8 06-JUN-2000;
 FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCCTCTCTCCAG 521
 |||||
 Db 9 TCCTCTCTCCAG 20

RESULT 167
 LOCUS AR097385/C 20 bp DNA PAT 14-FEB-2001
 DEFINITION Sequence 9 from patent US 6071726.
 ACCESSION AR097385
 VERSION AR097385.1 GI:12806115
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Diamandis,E., Dunn,J.M. and Stevens,J.K.
 TITLE Method, reagents and kit for diagnosis and targeted screening for
 p53 mutations
 JOURNAL Patent: US 6071726-A 9 06-JUN-2000;
 FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCCTCTCTCCAG 521
 |||||
 Db 18 TCCTCTCTCCAG 7

RESULT 168
 LOCUS AR099487 20 bp DNA PAT 14-FEB-2001
 DEFINITION Sequence 14 from patent US 6077833.
 ACCESSION AR099487
 VERSION AR099487.1 GI:12809253
 KEYWORDS
 SOURCE Unknown.

ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett,C.Frank. and Vickers,T.A.
 TITLE Oligonucleotide compositions and methods for the modulation of the
 expression of B7 protein
 JOURNAL Patent: US 6077833-A 14 20-JUN-2000;
 FEATURES Location/Qualifiers
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 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGAGCCCC 258
 |||||
 Db 6 TCCTGAGCCCC 17

RESULT 169
 LOCUS AR137400 20 bp DNA PAT 16-JUN-2001
 DEFINITION Sequence 15 from patent US 6197507.
 ACCESSION AR137400
 VERSION AR137400.1 GI:14478909
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Berg,T., Tollerud,O.Kristien. and Nilsen,O.
 TITLE Genetic test for alpha-mannosidosis
 JOURNAL Patent: US 6197507-A 15 06-MAR-2001;
 FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 378 GCGGCGGCTCA 389
 |||||
 Db 7 GCGGCGGCTCA 18

RESULT 170
 LOCUS AR143130 20 bp DNA PAT 08-AUG-2001
 DEFINITION Sequence 21 from patent US 6204055.
 ACCESSION AR143130
 VERSION AR143130.1 GI:15104416
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Dean,N.M. and Marcuseon,E.G.
 TITLE Antisense inhibition of Fas mediated signaling
 JOURNAL Patent: US 6204055-A 21 20-MAR-2001;
 FEATURES Location/Qualifiers
 1..20
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.0%; Score 12; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred.No. 9.1e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 GGAAATGCTCTT 182
|||||
20 GGAAATGCTCTT 9

Db 20 GGAAATGCTCTT 9

RESULT 171
AR178768 20 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 14 from patent US 6319906.
DEFINITION AR178768
ACCESSION AR178768
VERSION AR178768.1 GI:20219906
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
JOURNAL Patent: US 6319906-A 14-20-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
|||||
6 TCCTGGAGCCCC 17

Db 6 TCCTGGAGCCCC 17

RESULT 172
AR178952 20 bp DNA linear PAT 20-APR-2002
LOCUS Sequence 198 from patent US 6319906.
DEFINITION AR178952
ACCESSION AR178952
VERSION AR178952.1 GI:20220090
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Vickers,T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the expression of B7 protein
JOURNAL Patent: US 6319906-A 198-20-NOV-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGGAGCCCC 258
|||||
5 TCCTGGAGCCCC 16

Db 5 TCCTGGAGCCCC 16

RESULT 173
BD230144/c 20 bp DNA linear PAT 17-JUL-2003
LOCUS Total genome radiation hybrid map of canine genome and its use for identification of interesting genes.
DEFINITION BD230144
ACCESSION BD230144

VERSION BD230144.1 GI:33039914
KEYWORDS JP 2002530091-A/13.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris

REFERENCE
AUTHORS Galibert,F. and Andre,C.
TITLE 1 (bases 1 to 20)
JOURNAL Total genome radiation hybrid map of canine genome and its use for identification of interesting genes
COMMENT Patent: JP 2002530091-A 13-17-SEP-2002;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
OS Canis familiaris (dog)
PN JP 2002530091-A/13
PD 17-SEP-2002
PF 15-NOV-1999 JP 2000582596
PI 13-NOV-1998 US 60/108193
PI FRANCIS GALIBERT,CATHERINE ANDRE
PC C12N15/09,C12Q1/68,C12N15/00
CC Rem1023
FH key Location/Qualifiers
FT source 1..20
/organism="Canis familiaris (dog)".
Location/Qualifiers
1..20
/organism="genomic DNA"
/db_xref="taxon:9615"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 GGAGGGCTGCA 497
|||||
17 GGAGGGCTGCA 6

Db 17 GGAGGGCTGCA 6

RESULT 174
BD249305 20 bp DNA linear PAT 17-JUL-2003
LOCUS Antisense modulation of FAS mediated signaling.
DEFINITION BD249305/c
ACCESSION BD249305
VERSION BD249305.1 GI:33059075
KEYWORDS JP 2002540812-A/20.
SOURCE synthetic construct
ORGANISM artificial construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Marcussen,E.G.
TITLE Antisense modulation of FAS mediated signaling
JOURNAL Patent: JP 2002540812-A 20-03-DEC-2002;
ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002540812-A/20
PD 03-DEC-2002
PF 10-APR-2000 JP 2000610483
PR 12-APR-1999 US 09/290640
PI NICHOLAS M DEAN,ERIC G MARCUSSEN
PC C12N15/09,A61K31/7088,A61K31/7115,A61K31/712,A61K31/7125,PC
A61K48/00,
PC A61P1/16,A61P29/00,A61P35/00,A61P37/00,A61P43/00//C12N5/06,PC
C12N15/00,
CC C12N5/00
PC Synthetic Sequence
FH key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"

ORIGIN

Query Match	2.0%;	Score 12;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 9.1e+05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	171	GGAATGCTCTT	182
Db	20	GGAATGCTCTT	9

RESULT 175
FOC107

LOCUS	E06107	20 bp	DNA	linear	PAT 29-SEP-1997
DEFINITION	Oligonucleotide specific to subtype Pt of Hepatitis C virus.				
ACCESSION	F06107				

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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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Query Match	2.0%	Score 12;	DB 6;	Length 20;
Best Local Similarity	100.0%	Pred. No.	9.1e+05;	
Matches	12;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY	36	TTACCAATTCAA	47
Db	8	TTACCAATTCAA	19

RESULT	176			
125689				
LOCUS	125689	20 bp	DNA	linear
DEFINITION	Sequence 8 from patent US 5552283.			
ACCESSION	125689			
VERSION	125689.1	GI:160559		

JOURNAL	Patent: US 5552283-A 8 03-SEP-1996;
FEATURES	Location/Qualifiers
SOURCE	1. .20

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ORIGIN
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      2.0%  Score 12;  DB 6;  Length 20;
Best Local Similarity 100.0%;  Pred. 0.91e+05;
Matches 12;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 510 TCGTCTCTCCAG 521
|||
Db 9 TCGTCTCTCCAG 20

RESULT	177		
125690/c			
LOCUS	125690	20 bp	DNA
DEFINITION	Sequence 9 from patent US 5552283.		linear
FEATURES			
ORIGIN			
1			
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127			
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129			

ORIGIN	
Query Match	2.0%; Score 12; DB 6; Length 20;
Best Local Similarity	100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||
Db 18 TCGTCTCTCCAG 7

RESULT	178				
LOCUS	143305/c				
DEFINITION	143305	20 bp	DNA	linear	PAT 07-OCT-1997
ACCESSION	143305	Sequence 123	from patent	US 5631146.	
VERSION	143305.1	GI:2468549			
KEYWORDS	.				

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1: 20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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Query Match	2.0%	Score 12;	DB 6;	Length 20;
Best Local Similarity	100.0%	Pred. No. 3.1e+05;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	180	CTTCCTCCGCTA	191
Db	16	CTTCCTCCGCTA	5

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RESULT 179
AR206720      20 bp   DNA      linear   PAT 20-JUN-2002
LOCUS         AR206720
DEFINITION   Sequence 1 from patent US 6372436.
ACCESSION    AR206720
VERSION      AR206720.1 GI:21505407
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Pouzyrev,A.,Timofeyevich, and Riddle,D.Iee.
TITLE       Method for construction of cDNA libraries enriched in clones
corresponding to rare mRNA
JOURNAL      Patent: US 6372436-A 1 16-APR-2002;
FEATURES
SOURCE       1..20
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      246 CCGCTGGAGCCC 257
Db      1 CTCCTGGAGCCC 12

RESULT 180
AR265991      20 bp   DNA      linear   PAT 10-APR-2003
LOCUS         AR265991
DEFINITION   Sequence 172 from patent US 6492170.
ACCESSION    AR265991
VERSION      AR265991.1 GI:29694837
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Watt,A.T.
TITLE       Antisense modulation of caspase 9 expression
JOURNAL      Patent: US 6492170-A 172 10-DEC-2002;
FEATURES
SOURCE       1..20
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 CCGGAGGAGCTT 32
Db      5 CCGGAGGAGCTT 16

RESULT 181
AR281883      20 bp   DNA      linear   PAT 10-APR-2003
LOCUS         AR281883
DEFINITION   Sequence 6 from patent US 6521407.
ACCESSION    AR281883
VERSION      AR281883.1 GI:29717811
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Warentius,H.M. and Seabra,L.A.
TITLE       Methods for determining chemosensitivity of cancer cells based upon
expression of negative and positive signal transduction factors

```

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JOURNAL      Patent: US 6521407-A 6 18-FEB-2003;
FEATURES
SOURCE       1..20
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      510 TCGTCTCTCCAG 521
Db      9 TCGTCTCTCCAG 20

RESULT 182
AR299997/c    20 bp   DNA      linear   PAT 12-JUN-2003
LOCUS         AR299997/c
DEFINITION   Sequence 11732 from patent US 6537751.
ACCESSION    AR299997
VERSION      AR299997.1 GI:31687281
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE       Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL      Patent: US 6537751-A 11732 25-MAR-2003;
FEATURES
SOURCE       1..20
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      511 CGTCTCTCCAGA 522
Db      14 CGTCTCTCCAGA 3

RESULT 183
AR310801      20 bp   DNA      linear   PAT 12-JUN-2003
LOCUS         AR310801
DEFINITION   Sequence 1338 from patent US 6559294.
ACCESSION    AR310801
VERSION      AR310801.1 GI:31704227
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Griffiths,R., Holseth,S.K., Zagursky,R.J., Metcalfe,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE       Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL      Patent: US 6559294-A 1338 06-MAY-2003;
FEATURES
SOURCE       1..20
/mol_type="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      316 CTGAGATCTTC 327
Db      11 CTGAGATCTTC 327

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Db 9 CTGAGGATCTTC 20

RESULT 184
AR337679
LOCUS AR337679 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 14 from patent US 6566514.
ACCESSION AR337679
VERSION AR337679.1 GI:33724247
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE Oligonucleotide sequences complementary to thioredoxin or thioredoxin reductase genes and methods of using same to modulate cell growth
JOURNAL Patent: US 6566514-A 14 20-MAY-2003;
FEATURES
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 442 TCGAATCTTT 453
Db 7 TCGAATCTTT 18

RESULT 185
AR432224
LOCUS AR432224 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 21 from patent US 6653133.
ACCESSION AR432224
VERSION AR432224.1 GI:40194497
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M., Marcusson,E.G. and Wyatt,J.
TITLE Antisense modulation of Fas mediated signaling
JOURNAL Patent: US 6653133-A 21 25-NOV-2003;
FEATURES
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 171 GGAATGCTCTT 182
Db 20 GGAATGCTCTT 9

RESULT 186
AR437041
LOCUS AR437041 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 93 from patent US 6656732.
ACCESSION AR437041
VERSION AR437041.1 GI:40200125
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Bennett,C.F. and Watt,A.T.
TITLE Antisense inhibition of src-c expression
JOURNAL Patent: US 6656732-A 93 02-DEC-2003;
FEATURES
Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 280 GTGGCCGACTTT 291
Db 15 GTGGCCGACTTT 4

RESULT 187
AX018874
LOCUS AX018874 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO942839.
ACCESSION AX018874
VERSION AX018874.1 GI:10042970
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Warentus,H.
TITLE Treating cancer
JOURNAL Patent: WO 942839-A 6 26-AUG-1999;
THERYTE LIMITED (GB); WARENTUS HILMAR (GB)
FEATURES
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred.No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 510 TCCTCTCTCCAG 521
Db 9 TCCTCTCTCCAG 20

RESULT 188
AX018889
LOCUS AX018889 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO942834.
ACCESSION AX018889
VERSION AX018889.1 GI:10042985
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warentus,H.
TITLE Treating cancer
JOURNAL Patent: WO 942834-A 6 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENTUS HILMAR (GB)
FEATURES
Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
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Db 9 TCGTCTCTCCAG 20

RESULT 189

AX018906 20 bp DNA linear PAT 07-SEP-2000
LOCUS AX018906
DEFINITION Sequence 6 from Patent WO9942828.
ACCESSION AX018906
VERSION AX018906.1 GI:10043000
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942828-A 6 26-AUG-1999;
THERYTE LIMITED (GB); WARENITUS HILMAR MEEK (GB)
Location/Qualifiers
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
Db 9 TCGTCTCTCCAG 20

RESULT 190

AX018921 20 bp DNA linear PAT 07-SEP-2000
LOCUS AX018921
DEFINITION Sequence 6 from Patent WO9942821.
ACCESSION AX018921
VERSION AX018921.1 GI:10043016
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Seabra,L.A. and Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942821-A 6 26-AUG-1999;
SEABRA LAURENCE ANTHONY (GB); THERYTE LIMITED (GB); WARENITUS HILMAR MEEK (GB)
Location/Qualifiers
1.20
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||

Db 9 TCGTCTCTCCAG 20

RESULT 191
AX019035 20 bp DNA linear PAT 07-SEP-2000
LOCUS AX019035
DEFINITION Sequence 6 from Patent WO9942090.
ACCESSION AX019035
VERSION AX019035.1 GI:10043116
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Warenius,H.M.
TITLE Treating cancer
JOURNAL Patent: WO 9942090-A 6 26-AUG-1999;
THERYTE LIMITED (GB); WARENITUS HILMAR MEEK (GB)
Location/Qualifiers
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PRIMER"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
|||||
Db 9 TCGTCTCTCCAG 20

RESULT 192
AX293651 20 bp DNA linear PAT 21-NOV-2001
LOCUS AX293651
DEFINITION Sequence 5413 from Patent WO0179548.
ACCESSION AX293651
VERSION AX293651.1 GI:17055334
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Barany,F., Zivri,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE Method of designing addressable array for detection of nucleic acid
JOURNAL sequence differences using ligase detection reaction
Patent: WO 0179548-A 5413-25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
Location/Qualifiers
1.20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 ACCTACCTGTGC 90
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Db 9 ACCTACCTGTGC 20

RESULT 193
AX293867 20 bp DNA linear PAT 21-NOV-2001
LOCUS AX293867/c
DEFINITION Sequence 5629 from Patent WO0179548.
ACCESSION AX293867

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VERSION      AX293867.1 GI:17055550
KEYWORDS
SOURCE       synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE        Method of designing addressable array for detection of nucleic acid
              sequence differences using ligase detection reaction
JOURNAL      Patent: WO 0179548-A 5629 25-OCT-2001;
              CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
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              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Hypothetical Probe Sequence"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          52 GTCCGCTG33CT 63
              |||||
              |||||
Db          12 GTCCGCTG33CT 1
RESULT 194
AX295341/c   AX295341 20 bp DNA linear PAT 21-NOV-2001
LOCUS        Sequence 7103 from Patent WO0179548.
DEFINITION   AX295341
ACCESSION    AX295341
VERSION      AX295341.1 GI:17057030
KEYWORDS
SOURCE       synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.
TITLE        Method of designing addressable array for detection of nucleic acid
              sequence differences using ligase detection reaction
JOURNAL      Patent: WO 0179548-A 7103 25-OCT-2001;
              CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
  source     1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Hypothetical Probe Sequence"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          154 AAGACGCGCTGC 165
              |||||
              |||||
Db          19 AAGACGCGCTGC 8
RESULT 195
AX297041/c   AX297041 20 bp DNA linear PAT 21-NOV-2001
LOCUS        Sequence 8803 from Patent WO0179548.
DEFINITION   AX297041
ACCESSION    AX297041
VERSION      AX297041.1 GI:17058732
KEYWORDS
SOURCE       synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Barany,F., Zivvi,M., Gerry,N.P., Favis,R. and Kliman,R.

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TITLE        Method of designing addressable array for detection of nucleic acid
              sequence differences using ligase detection reaction
JOURNAL      Patent: WO 0179548-A 8803 25-OCT-2001;
              CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES
  source     1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Hypothetical Probe Sequence"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          584 CTTGGGACTTT 595
              |||||
              |||||
Db          20 CTTGGGACTTT 9
RESULT 196
AX301845     AX301845 20 bp DNA linear PAT 30-NOV-2001
LOCUS        Sequence 6 from Patent WO0185917.
DEFINITION   AX301845
ACCESSION    AX301845
VERSION      AX301845.1 GI:17382902
KEYWORDS
SOURCE       synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE    1
AUTHORS      Abduldayel,I.M.
TITLE        A device
JOURNAL      Patent: WO 0185917-A 6 15-NOV-2001;
              Tristem Ireland Limited (IE)
FEATURES
  source     1..20
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="primer"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY          317 TGAGATCTTCA 328
              |||||
              |||||
Db          5 TGAGATCTTCA 16
RESULT 197
AX459997     AX459997 20 bp DNA linear PAT 08-JUL-2002
LOCUS        Sequence 8 from Patent WO0203849.
DEFINITION   AX459997
ACCESSION    AX459997
VERSION      AX459997.1 GI:21725730
KEYWORDS
SOURCE       Homo sapiens (human)
              Homo sapiens
              Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1
AUTHORS      Schena,M.A.
TITLE        Microarray method of genotyping multiple samples at multiple loci
JOURNAL      Patent: WO 0203849-A 8 17-JUN-2002;
              Telechem International, Inc. (US)
FEATURES
  source     1..20
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"

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misc_feature 1 /db_xref="taxon:9606"
ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 249 CTGGAGCCCGCTG 260
7 CTGGAGCCCGCTG 18

RESULT 198
AX613711 20 bp DNA linear PAT 17-FEB-2003
LOCUS AX613711
DEFINITION Sequence 4736 from Patent WO02072882.
ACCESSION AX613711
VERSION AX613711.1 GI:28409140
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 Cullen, P. and Seedorf, U.
AUTHORS Coronary chip
JOURNAL Patent: WO 02072882-A 4736 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source 1.20
/mol_type="Homo sapiens"
/db_xref="taxon:9606"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 GCTGCCACGCTG 172
2 GCTGCCACGCTG 13

RESULT 199
AX710965 20 bp RNA linear PAT 11-APR-2003
LOCUS AX710965
DEFINITION Sequence 265 from Patent EP1288296.
ACCESSION AX710965
VERSION AX710965.1 GI:29787346
KEYWORDS
SOURCE Human herpesvirus 5
ORGANISM Human herpesvirus 5
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.

REFERENCE
1 Draper, K.G., McSwigen, J.A., Holecsek, J.J., Dudycz, L.W.,
AUTHORS Macejak, D.G., and Mamone, J.A.
JOURNAL Method and reagent for inhibiting HBV viral replication
Patent: EP 1288296-A 265 05-MAR-2003;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1.20
/mol_type="Human herpesvirus 5"
/db_xref="taxon:10359"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 223 TGCTACCGCGTC 234
DB 4 TGCTACCGCGTC 15

RESULT 200
BD001106 20 bp RNA linear PAT 31-JAN-2002
LOCUS BD001106
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001106
VERSION BD001106.1 GI:18625665
KEYWORDS UP 2000342285-A/266.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 (bases 1 to 20)
AUTHORS Draper, K.G., Dadykiz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holecsek, J.J., and Mamone, J.A.
JOURNAL Method and reagent for inhibiting viral replication
Patent: JP 2000342285-A 266 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Artificial Sequence
PN JP 2000342285-A/266
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132616
PF 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882828 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884433 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884521 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/935854 PR
14-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PR
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22//C12N5/10, C12R1:91, PC
C12N15/00
PC C12N5/00, C12N5/00, C12R1:91
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FT source 1.20
/mol_type="synthetic construct"
/db_xref="taxon:32630"

FEATURES
source 1.20
/mol_type="synthetic construct"
/db_xref="taxon:32630"

ORIGIN
Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 TGCTACCGCGTC 234
DB 4 TGCTACCGCGTC 15

RESULT 201
BD001535 20 bp RNA linear PAT 31-JAN-2002
LOCUS BD001535
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION BD001535
VERSION BD001535.1 GI:18626094
KEYWORDS UP 2000342286-A/266.

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ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1 (bases 1 to 20)
TITLE	Driper, K.G., Dadykztz, J.W., Macswigen, J.A., Mayesjak, D.G.,
JOURNAL	Hotseker, J.J. and Mamone, A.J.
COMMENT	Method and reagent for inhibiting viral replication
	Patent: JP 2000342286-A 266 12-DEC-2000;
	RIBOZYME PHARMACEUTICALS INC
	OS Artificial Sequence
	PN JP 2000342286-A/266
	PD 12-DEC-2000
	PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
	14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
	14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
	14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
	14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882971 PR
	14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR
	14-MAY-1992 US 07/883842, 14-MAY-1992 US 07/884073 PR
	14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
	14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
	14-MAY-1992 US 07/884336, 14-MAY-1992 US 07/884521 PR
	31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
	26-AUG-1992 US 07/935856, 18-SEP-1992 US 07/948359 PR
	15-OCT-1992 US 07/965322, 07-DEC-1992 US 07/987129 PR
	07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
	KENNETH G DRAVER, LEC W DADYKZT, JAMES A MACSWIGEN, PI DENNIS G
	MAYESJAK,
PI	JAMES J HOTSEKER, ANTHONY J MAMONE
PC	C12N15/09, C12N15/10, C12N7/00//A61K38/43, A61K39/125, A61K39/13,
PC	A61K39/135,
PC	A61K39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K48/00,
PC	A61P/16,
PC	A61P1/14, A61P1/16, A61P1/18, A61P1/22, A61P5/02, C12O1/68, PC
	(C12M15/09, C12N1/93), C12N15/00, C12N5/00, A61K37/48, (C12M15/00, PC
	C12R1/93)
CC	
FE	Key
FT	source
FT	1.20
FT	Location/Qualifiers
FT	Location/Qualifiers
FT	1.20
FT	/organism="synthetic construct"
FT	/mol_type="genomic RNA"
FT	/db_xref="taxon:33630"
FEATURES	
source	
ORIGIN	
Query Match	2.0%; Score 12; DB 6; Length 20;
Best Local Similarity	100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	223 TGCTACCGCGCTC 234
	4 TGCTACCGCGCTC 15
LOCUS	BD071075 20 bp DNA linear PAT 27-AUG-2002
DEFINITION	Modulation of mammalian telomerase by peptide nucleic acids.
ACCESSION	BD071075
VERSION	BD071075.1 GI:2261678
KEYWORDS	JP 2001517929-A/41.
SOURCE	JP 2001517929-A/41.
ORGANISM	unidentified
	unidentified
	unclassified.
REFERENCE	1 (bases 1 to 20)
AUTHORS	Shay, J.W., Wright, W.E., Piatyszek, M.A., Corey, D. and Nordon, J.C.
TITLE	Modulation of mammalian telomerase by peptide nucleic acids
JOURNAL	Parent: JP 2001517929-A 41 09-OCT-2001;
COMMENT	GERON CORP
	OS Unidentified

[illegible]

Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
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1 AGGATCTTCACC 12

RESULT 204
BD088443 20 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION BD088443
ACCESSION BD088443.1 GI:22634053
VERSION
KEYWORDS JP 2001321190-A/687.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)

REFERENCE
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 687 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA

COMMENT
OS Artificial Sequence
PN JP 2001321190-A/687
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA

PC C12N15/09,C12N15/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
Location/Qualifiers
1..20
Location/Qualifiers
/organism='Artificial Sequence'.
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 338 TCTACTCTGTG 349
|||||
12 TCTACTCTGTG 1

RESULT 205
BD089179 20 bp DNA linear PAT 27-AUG-2002
LOCUS A method of arraying genome clone.
DEFINITION BD089179
ACCESSION BD089179
VERSION BD089179.1 GI:22634789
KEYWORDS JP 2001321190-A/1423.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1 (bases 1 to 20)

REFERENCE
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 1423 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
GENOTECHS
COMMENT
OS Artificial Sequence
PN JP 2001321190-A/1423
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA

PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
C12N15/00,
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
Location/Qualifiers
FT source 1..20
Location/Qualifiers
/organism='Artificial Sequence'.
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 494 TGCATGAAATT 505
|||||
8 TGCATGAAATT 19

RESULT 206
BD131952 20 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION BD131952
Oligonucleotide sequence complementary to thioredoxin gene or
thioredoxin reductase gene and utilization thereof for controlling
cell proliferation.
BD131952
ACCESSION BD131952.1 GI:23226897
VERSION
KEYWORDS JP 2002501743-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Wright,J.A., Young,A.H. and Lee,Y.S.
TITLE 1 (bases 1 to 20)
JOURNAL Oligonucleotide sequence complementary to thioredoxin gene or
thioredoxin reductase gene and utilization thereof for controlling
Patent: JP 2002501743-A 14 22-JAN-2002;
GENESENSE TECHNOLOGIES INC

COMMENT
OS Homo sapiens (human)
PN JP 2002501743-A/14
PD 22-JAN-2002
PF 29-JAN-1999 JP 2000529423
PR 30-JAN-1998 US 60/073196
PI JIM A WRIGHT,ALPING H YOUNG,YOON S LEE
PC C12N15/09,A61K31/711,A61K48/00,A61P35/00,A61P35/04,C07H21/04//
PC (A61K31/711,A61K45/00),(A61K48/00,A61K45/00),C12N15/00 CC
Oligonucleotide sequence complementary to thioredoxin gene or CC
thioredoxin
CC reductase gene and utilization thereof for controlling cell
CC proliferation
FH Key Location/Qualifiers
FT source 1..20
Location/Qualifiers
/organism='Homo sapiens (human)'.
1..20
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN

Query Match 2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TGGATATCTTT 453
|||||
7 TGGATATCTTT 18

LOCUS	BD135497	20 bp	DNA		PAT 18-SEP-2002					
DEFINITION	Methods for analyzing animal products.									
ACCESSION	BD135497									
VERSION	BD135497.1	GI:23230442								
KEYWORDS	JP 2002504814-A/35.									
SOURCE	unidentified									
ORGANISM	unclassified.									
REFERENCE	1 (bases 1 to 20)									
AUTHORS	Andersson,L., Kijas,J., Giuffra,E., Jon,G., Evans,Wales,R. and Plastow,G.S.									
TITLE	Methods for analyzing animal products									
JOURNAL	Patent: JP 2002504814-A 35 12-FEB-2002;									
COMMENT	PIG IMPROVEMENT CO UK LTD									
OS	Unidentified									
PN	JP 2002504814-A/35									
PD	12-FEB-2002									
PF	27-MAY-1998 JP 1995500368									
PR	30-MAY-1997 GB 5711214.8, 31-JAN-1998 GB				9801990.4 PI					
LEIF	ANDERSSON,JAMES KIJAS,ELISABETTA GIUFFRA,GARY JON PI									
EVANS,RICHARD WALES,										
PI	GRAHAM STUART PLASTOW									
PC	C12Q1/68									
CC	Strandedness: Single;									
CC	Topology: Linear;									
CC	Primer									
FH	Key	Location/Qualifiers								
FT	source	1..20								
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FEATURES	source	1..20								
		Location/Qualifiers								
		/organism="unidentified"								
		/mol_type="genomic DNA"								
		/db_xref="taxon:32644"								
ORIGIN										
	Query Match	2.0%;	Score 12;	DB 6;	Length 20;					
	Best Local Similarity	100.0%;	Pred. No. 9.1e+05;							
	Matches	12;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
OY	243	CACCTCCTGGAG	254							
DB	20	CACCTCCTGGAG	9							
RESULT	208									
	BD170190									
LOCUS	BD170190	20 bp	DNA		PAT 17-JAN-2003					
DEFINITION	Method of synthesizing single-stranded nucleic acid.									
ACCESSION	BD170190									
VERSION	BD170190.1	GI:27876002								
KEYWORDS	WO 0234907-A/22.									
SOURCE	WO 0234907-A/22.									
ORGANISM	synthetic construct									
	synthetic construct									
	artificial sequences.									
	1 (bases 1 to 20)									
REFERENCE	Nagamine,K., Hase,T. and Notomi,T.									
AUTHORS	Method of synthesizing single-stranded nucleic acid									
TITLE	Patent: WO 0234907-A 22 02-MAY-2002;									
JOURNAL	EIKEN CHEMICAL CO LTD,KENTARO NAGAMINE,TETSU HASE,TSUGUNORI NOTOMI									
COMMENT	OS Artificial Sequence									
	PN WO 0234907-A/22									
	PD 02-MAY-2002									
	PF 26-OCT-2001 WO 2001JP009452									
	PR 27-OCT-2000 JP 00P 328219									
	PI KENTARO NAGAMINE,TETSU HASE,TSUGUNORI NOTOMI									
	PC C12N15/10,C12Q1/68									
	CC Description of Artificial Sequence:Outer primer(Forward) FH									
	Key	Location/Qualifiers								
	FT	source	1..20							
		/organism='Artificial Sequence'.								

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FEATURES
source
1. .20
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

ORIGIN
Query Match      2.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      319 AGGATCTTCACC 330
      |||||
      7 AGGATCTTCACC 18

RESULT 209
AB068586      20 bp DNA linear SYN 21-MAY-2003
LOCUS
DEFINITION Synthetic construct DNA, forward primer for human STS sts-R90NSR at
ACCESSION AB068586
VERSION 1p36.
KEYWORDS
SOURCE
ORGANISM
AUTHORS
REFERENCE
1
Chen, Y.-Z., Hayashi, Y., Wu, J.-G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Mochizuki, A., Chira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.
and Soeda, E.
A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
Genomics 74 (1), 55-70 (2001)
2
11374902
2 (bases 1 to 20)
Horii, A.
Direct Submission
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Setiyomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
Location/Qualifiers
1. .20
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

misc_feature
1. .20
  /note="forward primer for human STS sts-R90NSR at 1p36
  sts-R90NSR obtained from clones B133M1, B369A24, B341P17,
  B26P12, B341P17, B3341L24, B12802, B90N5, B229F2, Human
  BAC library RPT-11"

ORIGIN
Query Match      2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      494 TGCATGAATTT 505
      |||||
      8 TGCATGAATTT 19

RESULT 210
AB069312      20 bp DNA linear SYN 21-MAY-2003
LOCUS
DEFINITION Synthetic construct DNA, forward primer for human STS sts-G13123
ACCESSION AB069312
VERSION 1p36.
KEYWORDS
SOURCE
ORGANISM
AUTHORS
REFERENCE
1
GI:15130116

```

```

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
            Matsubae, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
            Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, N., Horii, A.
            and Soeda, E.
TITLE       A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
JOURNAL     Genomics 74 (1), 55-70 (2001)
MEDLINE    21269192
PUBMED     11374902
REFERENCE   2 (bases 1 to 20)
AUTHORS     Horii, A.
TITLE       Direct Submission
JOURNAL     Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
            Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source      1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
misc_feature 1..20
            /note="forward primer for human STS sts-stsG3123 at 1p36
            sts-stsG3123 obtained from clones B157K6, B14F15, B21G9,
            B21F9, Human BAC library Rpci-11"

ORIGIN
Query Match      2.0%; Score 12; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 9, 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      338 TCTACTTCTGTG 349
DB      12 TCTACTTCTGTG 1

RESULT 211
AX627549
LOCUS      AX627549
DEFINITION Sequence 4590 from Patent WO02053774.
ACCESSION  AX627549
VERSION     AX627549.1 GI:28455587
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4590 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3, 3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      569 GAGACGATTT 579
DB      1 GAGACGATTT 11

RESULT 212

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AX628350/c
LOCUS      AX628350
DEFINITION Sequence 5391 from Patent WO02053774.
ACCESSION  AX628350
VERSION     AX628350.1 GI:28456388
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5391 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
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            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3, 3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      247 TCCTGAGAGCCC 257
DB      11 TCCTGAGAGCCC 1

RESULT 213
AX629660
LOCUS      AX629660
DEFINITION Sequence 6701 from Patent WO02053774.
ACCESSION  AX629660
VERSION     AX629660.1 GI:28457698
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn, D., Conrad, M. and Hofmann, K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6701 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 3, 3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      445 AATACCTTTGT 455
DB      1 AATACCTTTGT 11

RESULT 214
AX632806
LOCUS      AX632806
DEFINITION Sequence 9848 from Patent WO02053774.
ACCESSION  AX632806
VERSION     AX632806.1 GI:28466421
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9848 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 480 AGCCTGGAG 490
DB 1 AGCCTGGAG 11
RESULT 215
LOCUS AR058692 12 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 269 from patent US 5837832.
ACCESSION AR058692
VERSION AR058692.1 GI:5984269
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 12)
AUTHORS Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbard,E.A.,
Lipshutz,R.J., Lohman,P.E., Morris,M.S. and Sheldon,B.L.
TITLE Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 269 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 462 CCATGAAGA 472
DB 2 CCATGAAGA 12
RESULT 216
LOCUS BD242529 12 bp DNA linear PAT 17-JUL-2003
DEFINITION A system for cell based screening.
ACCESSION BD242529
VERSION BD242529.1 GI:33052299
KEYWORDS JP 2002528136-A/35.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 12)
AUTHORS Guiliano,K.A., Bright,G., Olson,K. and Tencza,S.B.
TITLE A system for cell based screening
JOURNAL Patent: JP 2002528136-A 35 03-SEP-2002;
CELLONICS INC
OS Artificial Sequence
PN JP 2002528136-A/35
PD 03-SEP-2002
PF 29-OCT-1999 JP 2000579780
PR 30-OCT-1998 US 60/106308,26-MAY-1999 US 60/136078 PI
KENNETH A.GUILIANO,GARY BRIGHT,KEITH OLSON,SARAH BURROUGHS PI

TENCZA
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/02,C12Q1/
PC 37,G01N33/15,
PC G01N33/50,C12N15/00,C12N5/00
CC Description of Artificial Sequence: proCaspase-6 substrate CC
recognition
CC sequence
FH Key Location/Qualifiers
FT source 1..12
/organism="Artificial Sequence".
FEATURES
source 1..12
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 338 TCTACTTCTGT 348
DB 11 TCTACTTCTGT 1
RESULT 217
LOCUS AR217454 12 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 69 from patent US 6416959.
ACCESSION AR217454
VERSION AR217454.1 GI:23317147
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 12)
AUTHORS Guiliano,K. and Kapur,R.
TITLE System for cell-based screening
JOURNAL Patent: US 6416959-A 69 09-JUL-2002;
FEATURES Location/Qualifiers
source 1..12
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 338 TCTACTTCTGT 348
DB 11 TCTACTTCTGT 1
RESULT 218
LOCUS AX766780 12 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 69 from Patent EP1314980.
ACCESSION AX766780
VERSION AX766780.1 GI:32260534
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Guiliano,K.A. and Kapur,R.
TITLE A system for cell-based screening
JOURNAL Patent: EP 1314980-A 69 28-MAY-2003;
CELLONICS, Inc. (US)
FEATURES Location/Qualifiers
source 1..12
/organism="synthetic construct"

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/moi_type="unassigned DNA"
/db_xref="taxon:32630"
/note="proCaspase-6 substrate recognition sequence"

ORIGIN

Query Match          1.8%; Score 11; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      338 TCTACTTCTGT 348
      |||||
      11 TCTACTTCTGT 1

RESULT 219
LOCUS      AX555912          13 bp      DNA      linear      PAT 27-NOV-2002
DEFINITION Sequence 508 from Patent WO02070755.
ACCESSION  AX555912
VERSION     AX555912.1 GI:25899370
KEYWORDS
SOURCE      synthetic construct
            synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Lyamichev,V.I., Kaiser,M.W. and Lyamicheva,N.
TITLE       Pen endonucleases
            Patent: WO 02070755-A 508 12-SEP-2002;
            Third Wave Technologies, Inc. (US)
FEATURES
            Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

ORIGIN

Query Match          1.8%; Score 11; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      101 AGAGCGCTGAC 111
      |||||
      13 AGAGCGCTGAC 3

RESULT 220
LOCUS      AJ598336          13 bp      DNA      linear      PLN 23-OCT-2003
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            466b02.
ACCESSION  AJ598336
VERSION     AJ598336.1 GI:37947964
KEYWORDS   right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE   1
AUTHORS     Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechold,N., Crenaud,C., Derose,R., Pelletier,G.,
            Lepoint,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMO Rep. 3 (12), 1152-1157 (2002)
MEDLINE    22363535
PUBMED     12446565
REFERENCE   2 (bases 1 to 13)
AUTHORS     Balzergue,S.
TITLE       Direct Substitution
JOURNAL     Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gascon Creneau, 91057 Evry cedex, FRANCE
COMMENT    PCR was performed on DNA from transformants of Arabidopsis thaliana

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FEATURES		plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/ . This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.inbio.gen.fr).	
source		Location/Qualifiers	
		1..13	
		/organism="Arabidopsis thaliana"	
		/mol_type="genomic DNA"	
		/cultivar="MassiliaewskiJa"	
		/db_xref="taxon:3702"	
		/clone="46D02"	
		/clone_1db="Arabidopsis thaliana T-DNA insertion lines"	
misc_feature		1..13	
		/note="T-DNA flanking sequence	
		right border"	
ORIGIN			
Query Match		1.8%; Score 11; DB 8; Length 13;	
Best Local Similarity		100.0%; Pred. No. 3,3e+06;	
Matches		11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	424 AAAGATTATTT 434		
DB	3 AAAGATTATTT 13		
RESULT 221			
LOCUS		A42580 14 bp DNA linear PAT 06-MAR-1997	
DEFINITION		Sequence 97 from Patent W09502061.	
ACCESSION		A42580	
VERSION		A42580.1 GI:2298029	
KEYWORDS			
SOURCE		. unidentified	
ORGANISM		unidentified	
REFERENCE		1 (bases 1 to 14)	
AUTHORS		Schlingensiepen,G., Schlingensiepen,R., Schlingensiepen,K. and Brysch,W.	
TITLE		A PHARMACEUTICAL COMPOSITION COMPRISING ANTISENSE-NUCLEIC ACID FOR PREVENTION AND/OR TREATMENT OF NEURONAL INJURY, DEGENERATION AND CELL DEATH AND FOR THE TREATMENT OF NEOPLASMS	
JOURNAL		Patent: WO 9502061-A, 97.19-JAN-1995;	
COMMENT		BIOGENOSTIK GBS FUER BIOMOLEKUL (DB)	
FEATURES		Other publication AU 7345694 950206.	
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		/organism="unidentified"	
		/mol_type="unassigned DNA"	
		/db_xref="taxon:32644"	
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Query Match		1.8%; Score 11; DB 6; Length 14;	
Best Local Similarity		100.0%; Pred. No. 3,3e+06;	
Matches		11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	413 TCATGACCTTC 423		
DB	2 TCATGACCTTC 12		
RESULT 222			
LOCUS		A88769 14 bp DNA linear PAT 22-JAN-2000	
DEFINITION		Sequence 917 from Patent W09833904.	
ACCESSION		A88769	
VERSION		A88769.1 GI:6737339	

KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1 (bases 1 to 14)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 917 06-AUG-1998;
BIOLOGISTIK GES. (DE); BRYSCH WOLFGANG (DE)
FEATURES
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Query Match 1.8%; Score 11; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 413 TCATGACCTTC 423
DB 2 TCATGACCTTC 12
RESULT 223
188009 14 bp DNA linear PAT 10-AUG-1998
LOCUS
DEFINITION Sequence 1 from patent US 5716835.
ACCESSION 188009
VERSION 188009.1 GI:3407949
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Regan, J. W., Gil, D. W. and Woodward, D. F.
TITLE Nucleic acid encoding a novel human EP prostaglandin receptor
JOURNAL Patent: US 5716835-A 1 10-FEB-1998;
FEATURES
source
1. .14
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 256
DB 3 CTCCTGAGGCC 13
RESULT 224
AR372103 14 bp DNA linear PAT 12-SEP-2003
LOCUS
DEFINITION AR372103 Sequence 1 from patent US 6395878.
ACCESSION AR372103
VERSION AR372103.1 GI:34609385
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Regan, J. W., Gil, D. W. and Woodward, D. F.
TITLE Nucleic acid encoding a human EP prostaglandin receptor
JOURNAL Patent: US 6395878-A 1 28-MAY-2002;
FEATURES
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1. .14
/organism="unknown"
/mol_type="genomic DNA"
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Query Match 1.8%; Score 11; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 256
DB 3 CTCCTGAGGCC 13
RESULT 225
AX133710/c 14 bp DNA linear PAT 15-MAY-2001
LOCUS
DEFINITION AX133710 Sequence 8 from Patent WO0130381.
ACCESSION AX133710
VERSION AX133710.1 GI:14139720
KEYWORDS
SOURCE
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Abarinejad, S.
TITLE Use of csf-1 inhibitors
JOURNAL Patent: WO 0130381-A 8 03-MAY-2001;
Hotbauer, Reinhold (AT)
FEATURES
source
1. .14
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 389 ACCGCGCCGGG 399
DB 12 ACCGCGCCGGG 2
RESULT 226
BD066282 14 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION BD066282 An antisense oligonucleotide preparation method.
ACCESSION BD066282
VERSION BD066282.1 GI:22611885
KEYWORDS JP 2001511000-A/917.
SOURCE unidentified
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Schlingensiepen, K. H. and Brysch, W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 917 07-AUG-2001;
BIOLOGISTIK GEBELTSCHAFT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT
OS Unknown
PN JP 2001511000-A/917
PD 07-AUG-2001
PF 30-JAN-1998 JP 199853253
PR 31-JAN-1997 EP 97101311.8
PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH
PC C12N15/11, C07H21/04, A61K31/70
CC An antisense oligonucleotide preparation method FH Key
FEATURES
source
1. .14
/organism="unknown"
Location/Qualifiers
FT source
1. .14
/organism="unknown"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 413 TCATGACCTTC 423
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 2 TCATGACCTTC 12

Db 2 TCATGACCTTC 12

RESULT 227
 BD201796/c
 LOCUS 14 bp RNA linear PAT 17-JUL-2003
 DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.

ACCESSION BD201796
 VERSION BD201796.1 GI:33011566
 KEYWORDS JP 2002509721-A/4822.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.
 TITLE 1 (bases 1 to 14)
 JOURNAL Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswigen, J.A.
 Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
 Patent: JP 2002509721-A 4822 02-APR-2002;

COMMENT RIBOZYME PHARMACEUTICALS INC

OS Homo sapiens (human)
 PN JP 2002509721-A/4822
 PD 02-APR-2002
 PF 24-MAR-1998 JP 2000541291
 PR 27-MAR-1998 US 60/079678
 PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
 PI JAMES A MCSWIGEN

PC C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
 A61P29/00, A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
 C12N5/00

CC Method and reagent for treating diseases or conditions CC
 concerning molecule
 CC participating in vasculogenic response
 FH Key Location/Qualifiers
 FT source 1.14
 /organism='Homo sapiens (human)'

FEATURES
 source 1.14
 Location/Qualifiers
 /organism='Homo sapiens'
 /mol_type='genomic RNA'
 /db_xref='taxon:9606'

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 221 GCTGCTACCGC 231
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 13 GCTGCTACCGC 3

Db 13 GCTGCTACCGC 3

RESULT 228
 BD209325
 LOCUS 14 bp RNA linear PAT 17-JUL-2003
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.

ACCESSION BD209325
 VERSION BD209325.1 GI:33019095
 KEYWORDS JP 2002512791-A/2915.
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE
 AUTHORS unclassified.
 TITLE 1 (bases 1 to 14)
 JOURNAL Blatt, L., Mcswigen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
 Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
 Patent: JP 2002512791-A 2915 08-MAY-2002;

COMMENT RIBOZYME PHARMACEUTICALS INC
 OS Hepatitis virus (hepatitis C virus)
 PN JP 2002512791-A/2915
 PD 08-MAY-2002
 PF 26-APR-1998 JP 2000545991
 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR
 25-FEB-1999 US 09/27608, 23-MAR-1999 US 09/274553 PI
 LAWRENCE BLATT, JAMES A MCSWIGEN, ELISABETH ROBERTS, PAMELA A PI
 PAVCO.

PI DENNIS MACEJAK
 PC C12N9/00, A61K31/7105, A61K38/21, A61K48/00, A61P31/12, C12N15/09,
 PC A61K37/06,
 PC C12N15/00

CC Enzymatic nucleic acid treatment of diseases or conditions CC
 related to
 CC hepatitis C virus infection.
 FH Key Location/Qualifiers
 FT source 1.14
 /organism='Hepatitis virus (hepatitis C FT
 virus)'

FEATURES
 source 1.14
 Location/Qualifiers
 /organism='unidentified'
 /mol_type='genomic RNA'
 /db_xref='taxon:32644'

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 216 TGGCCGCTGCT 226
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 1 TGGCCGCTGCT 11

RESULT 229
 AR033266/c
 LOCUS 15 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 32 from patent US 5869253.
 ACCESSION AR033266
 VERSION AR033266.1 GI:5948871

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE
 AUTHORS 1 (bases 1 to 15)
 TITLE Draper, K.G.
 JOURNAL Method and reagent for inhibiting hepatitis C virus replication
 Patent: US 5869253-A 32 09-FEB-1999;

FEATURES
 source 1.15
 Location/Qualifiers
 /organism='unknown'
 /mol_type='unassigned DNA'

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369
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 13 AGGCTGAGCCC 3

Db 13 AGGCTGAGCCC 3

RESULT 230
 AR056295

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LOCUS       AR056295                15 bp    DNA                linear    PAT 29-SEP-1999
DEFINITION   Sequence 499 from patent US 5837542.
ACCESSION    AR056295
VERSION      AR056295.1  GI:5981872
KEYWORDS     SOURCE
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 499 17-NOV-1998;
            Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244  ACCTCCTGGAG 254
DB      4  ACCTCCTGGAG 14

RESULT 231
LOCUS       AR056484                15 bp    DNA                linear    PAT 29-SEP-1999
DEFINITION   Sequence 688 from patent US 5837542.
ACCESSION    AR056484
VERSION      AR056484.1  GI:5982061
KEYWORDS     SOURCE
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 688 17-NOV-1998;
            Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244  ACCTCCTGGAG 254
DB      4  ACCTCCTGGAG 14

RESULT 232
LOCUS       AR056532                15 bp    DNA                linear    PAT 29-SEP-1999
DEFINITION   Sequence 736 from patent US 5837542.
ACCESSION    AR056532
VERSION      AR056532.1  GI:5982109
KEYWORDS     SOURCE
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
            Draper,K.G.
TITLE       Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL     Patent: US 5837542-A 736 17-NOV-1998;
            Location/Qualifiers
            1..15
            /organism="unknown"
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ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244  ACCTCCTGGAG 254
DB      4  ACCTCCTGGAG 14

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FEATURES
Source
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244  ACCTCCTGGAG 254
DB      4  ACCTCCTGGAG 14

RESULT 233
LOCUS       AR071434                15 bp    DNA                linear    PAT 18-FEB-2000
DEFINITION   Sequence 31 from patent US 5910626.
ACCESSION    AR071434
VERSION      AR071434.1  GI:7222322
KEYWORDS     SOURCE
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Haselkorn,R. and Gornicki,P.
TITLE       Acetyl-CoA carboxylase compositions and methods of use
JOURNAL     Patent: US 5910626-A 31 08-JUN-1999;
            Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      555  GGTTGATGACT 565
DB      4  GGTTGATGACT 14

RESULT 234
LOCUS       AR113088/c              15 bp    DNA                linear    PAT 16-MAY-2001
DEFINITION   Sequence 32 from patent US 6132966.
ACCESSION    AR113088
VERSION      AR113088.1  GI:14093410
KEYWORDS     SOURCE
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Draper,K.G.
TITLE       Method and reagent for inhibiting hepatitis C virus replication
JOURNAL     Patent: US 6132966-A 32 17-OCT-2000;
            Location/Qualifiers
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Query Match      1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      359  AGGCTGAGCCC 369
DB      13  AGGCTGAGCCC 3

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RESULT 235
AUTHORS AR114053 15 bp DNA linear PAT 16-MAY-2001
LOCUS AR114053
DEFINITION Sequence 499 from patent US 6132967.
ACCESSION AR114053
VERSION AR114053.1 GI:114094375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
Unclassified.
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 499 17-OCT-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
4 ACCTCCTGGAG 14

RESULT 236
LOCUS AR114242 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 688 from patent US 6132967.
ACCESSION AR114242
VERSION AR114242.1 GI:14094564
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
Unclassified.
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 688 17-OCT-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
4 ACCTCCTGGAG 14

RESULT 237
LOCUS AR114290 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 736 from patent US 6132967.
ACCESSION AR114290
VERSION AR114290.1 GI:14094612
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
Unclassified.

AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 736 17-OCT-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
4 ACCTCCTGGAG 14

RESULT 238
LOCUS AR132197 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 622 from patent US 6194150.
ACCESSION AR132197
VERSION AR132197.1 GI:14121102
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
Unclassified.
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 622 27-FEB-2001;
FEATURES Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 418 ACCTCAAGA 428
|||||
4 ACCTCAAGA 14

RESULT 239
LOCUS AR132198 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 623 from patent US 6194150.
ACCESSION AR132198
VERSION AR132198.1 GI:14121103
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
Unclassified.
AUTHORS Stinchcomb,D.T., Jarvis,T. and McSwiggen,J.
TITLE Nucleic acid based inhibition of CD40
JOURNAL Patent: US 6194150-A 623 27-FEB-2001;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	418	ACCTTCAAGA	428
Db	4	ACCTTCAAGA	14

RESULT	240
ARI32199	
LOCUS	ARI32199
DEFINITION	Sequence 624 from patent US 6194150.
Accession	U000000000
	15 bp DNA linear PAT 16-MAY-2001

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/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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RESULT 241	
ARI32200	15 bp DNA linear PAT 16-MAY-2001
LOCUS	ARI32200
DEFINITION	Sequence 625 from patent US 6194150.
ACCESSION	ARI32200
VERSION	ARI32200.1 GI:14121105
ORIGIN	

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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match          1.8%  Score 11;  DB 6;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 3.3e+06;
Matches 11;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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RESULT	242		
LOCUS	AR133396		
DEFINITION	Sequence 1821 from patent US 6194150.	15 bp	DNA
ACCESSION	AR133396		linear
VERSION	AR133396.1		PAT 16-MAY-2001
KEYWORDS	GI:14122301		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		

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REFERENCE      1 (bases 1 to 15)
AUTHORS        Stinchcomb,D.T., Jarvis,T. and McSwiggen,J
TITLE          Nucleic acid based inhibition of CD40
JOURNAL        Patent: US 6194150-A 1821 27-FEB-2001;
FEATURES       Location/Qualifiers
                1..15

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ORIGIN

Query Match	1.84	Score 11	DB 6	Length 15
Best Local Similarity	100.0%	Pred. No.	3.3e+05	
Matches 11	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 41 AATTCAAAAT 51
|||
Db 5 AATTCAAAAT 15

REFERENCE	Unclassified.
AUTHORS	1. (bases 1 to 15)
TITLE	Sin3hccomb.D.T., Jarvis, T. and McSwiggen, J
JOURNAL	Nucleic acid based inhibition of Cpd0
FEATURES	Patent: US 6194150-A 1992-27-FEB-2001;
source	Location/Qualifiers
	1..15

LOCUS	DEFINITION	ACCESSION	VERSION	RESULT 244
AR133398	Sequence 1823 from patent US 6194150.	AR133398	AR133398.1	GI:14122303
	15 bp	DNA	linear	PAT 16-MAY-2001

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ORIGIN                               /mol_type="unassigned DNA"
Query Match                         1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
                                41 AATTCAAAAT 51

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Db 5 AATTCAAAAAT 15

RESULT 245
LOCUS I30019 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5578714.
ACCESSION I30019
VERSION I30019.1 GI:1820810
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Pogo,A.O. and Chaudhuri,A.
TITLE DNA encoding Duffy spd protein
JOURNAL Patent: US 5578714-A 4 26-NOV-1996;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGCCTGGG 487
Db 15 CAAGCCTGGG 5

RESULT 246
LOCUS I39402 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 440 from patent US 5616488.
ACCESSION I39402
VERSION I39402.1 GI:2083882
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 440 01-APR-1997;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATCTT 451
Db 12 CTGGAATCTT 2

RESULT 247
LOCUS I39403 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 441 from patent US 5616488.
ACCESSION I39403
VERSION I39403.1 GI:2083883
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)

AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 441 01-APR-1997;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATCTT 451
Db 11 CTGGAATCTT 1

RESULT 248
LOCUS I39404 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 442 from patent US 5616488.
ACCESSION I39404
VERSION I39404.1 GI:2083884
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Sullivan,S., Draper,K.G., McSwiggen,J. and Stinchcomb,D.T.
TITLE IL-5 targeted ribozymes
JOURNAL Patent: US 5616488-A 442 01-APR-1997;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATCTT 451
Db 11 CTGGAATCTT 1

RESULT 249
LOCUS I57495 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 32 from patent US 5610054.
ACCESSION I57495
VERSION I57495.1 GI:2482559
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Enzymatic RNA molecule targeted against Hepatitis C virus
JOURNAL Patent: US 5610054-A 32 11-MAR-1997;
FEATURES
source
Location/Qualifiers
1. .15
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred.No.3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 AGGCTGAGCCC 369

Db 13 AGCGTGGAGCC 3

RESULT 250

LOCUS 171878

DEFINITION Sequence 4 from patent US 5683696.

ACCESSION 171878

VERSION 171878.1

KEYWORDS GI:3008017

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 15)

AUTHORS Pogo, A., Oscar, and Chaudhuri, A.

TITLE Cloning of Duffy blood group antigen, gpd

JOURNAL Patent: US 5683696-A 4 04-NOV-1997,

FEATURES

Source

1.15

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 477 CAAGGCTGGG 487

Db 15 CAAGGCTGGG 5

RESULT 251

LOCUS AX133713 15 bp DNA

DEFINITION Sequence 11 from Patent WO0130381.

ACCESSION AX133713

VERSION AX133713.1

KEYWORDS GI:14139723

SOURCE

ORGANISM

REFERENCE 1

AUTHORS Aharinejad, S.

TITLE Use of csi-1 inhibitors

JOURNAL Patent: WO 0130381-A 11 03-MAY-2001;

FEATURES

Source

1.15

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 389 ACCGCGCGCGG 399

Db 4 ACCGCGCGCGG 14

RESULT 252

LOCUS AX633447 15 bp RNA

DEFINITION Sequence 586 from Patent EP1260586.

ACCESSION AX633447

VERSION AX633447.1

KEYWORDS GI:28469061

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1

AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Dizenzo, A., Karpelsky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 586 27-NOV-2002;

FEATURES

Source

1.15

/organism="unidentified"

/mol_type="unassigned RNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGGAG 254

Db 4 ACCCTCTGGAG 14

RESULT 253

LOCUS AX633488 15 bp RNA

DEFINITION Sequence 627 from Patent EP1260586.

ACCESSION AX633488

VERSION AX633488.1

KEYWORDS GI:28469102

SOURCE

ORGANISM

REFERENCE 1

AUTHORS Stinchcomb, D.T., Dudycz, L.W., Chowrira, B., Grimm, S., Dizenzo, A., Karpelsky, A., Draper, K.G., Kisch, K., Matulic-Adamic, J., Mcswiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 627 27-NOV-2002;

FEATURES

Source

1.15

/organism="unidentified"

/mol_type="unassigned RNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCCTCTGGAG 254

Db 4 ACCCTCTGGAG 14

RESULT 254

LOCUS AX633547 15 bp RNA

DEFINITION Sequence 686 from Patent EP1260586.

ACCESSION AX633547

VERSION AX633547.1

KEYWORDS GI:28469161

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A., Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., Mswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 686 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
source location/Qualifiers
1.15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 244 ACCTCCTGGAG 254
Db 4 ACCTCCTGGAG 14
RESULT 255
AX635687/c 15 bp RNA linear PAT 24-FEB-2003
LOCUS AX635687
DEFINITION Sequence 2826 from Patent EP1260586.
ACCESSION AX635687
VERSION AX635687.1 GI:28471301
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A., Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., Mswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2826 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
source location/Qualifiers
1.15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTGGAACTACTT 451
Db 12 CTGGAACTACTT 2
RESULT 256
AX635689/c 15 bp RNA linear PAT 21-FEB-2003
LOCUS AX635689
DEFINITION Sequence 2828 from Patent EP1260586.
ACCESSION AX635689
VERSION AX635689.1 GI:28471303
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1

AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A., Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., Mswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2828 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
source location/Qualifiers
1.15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTGGAACTACTT 451
Db 11 CTGGAACTACTT 1
RESULT 257
AX635691/c 15 bp RNA linear PAT 21-FEB-2003
LOCUS AX635691
DEFINITION Sequence 2830 from Patent EP1260586.
ACCESSION AX635691
VERSION AX635691.1 GI:28471305
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A., Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J., Mswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 2830 27-NOV-2002;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US)
source location/Qualifiers
1.15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 441 CTGGAACTACTT 451
Db 11 CTGGAACTACTT 1
RESULT 258
BD206999/c 15 bp RNA linear PAT 17-UTL-2003
LOCUS BD206999
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD206999
VERSION BD206999.1 GI:33016769
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 15)

AUTHORS	Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
TITLE	Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL	Patent: JP 2002512791-A 589 08-MAY-2002; RIBOZYME PHARMACEUTICALS INC OS Hepatitis virus (hepatitis C virus) PN JP 2002512791-A/589
COMMENT	PD 08-MAY-2002 PR 26-APR-1999 JP 2000545991 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PAVCO, PI DENNIS MACEJAK PC C12N5/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09, PC A61K37/66, PC C12N15/00 CC Enzymatic nucleic acid treatment of diseases or conditions related to CC hepatitis C virus infection. FH key location/Qualifiers 1..15 FT source location/Qualifiers 1..15 virus'/organism='Hepatitis virus (hepatitis C virus)'
FEATURES	source location/Qualifiers 1..15 /organism="unidentified" /mol_type="genomic RNA" /db_xref="taxon:32644"
ORIGIN	
Query Match	1.8%; Score 11; DB 6; Length 15;
Best Local Similarity	100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Cy	359 AGCGTAGAGCCC 369
Db	13 AGGCTGAGCCCC 3
RESULT 259	
BD208353	15 bp RNA linear PAT 17-JUL-2003
LOCUS	
DEFINITION	Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION	BD208353
VERSION	BD208353.1 GI:33018123
KEYWORDS	JP 2002512791-A/1943.
SOURCE	unidentified
ORGANISM	unclassified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 15)
TITLE	Blatt, L., McSwiggen, J.A., Roberts, E., Pavco, P.A. and Macejak, D.
JOURNAL	Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
COMMENT	Patent: JP 2002512791-A 1943 08-MAY-2002; RIBOZYME PHARMACEUTICALS INC OS Hepatitis virus (hepatitis C virus) PN JP 2002512791-A/1943 PD 08-MAY-2002 PF 26-APR-1999 JP 2000545991 PR 27-APR-1998 US 60/083217, 18-SEP-1998 US 60/100842 PR 25-FEB-1999 US 09/257608, 23-MAR-1999 US 09/274553 PI LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PAVCO, PI DENNIS MACEJAK PC C12N5/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09, PC A61K37/66, PC C12N15/00 CC Enzymatic nucleic acid treatment of diseases or conditions related to CC hepatitis C virus infection. FH key location/Qualifiers

FT	source	1.15	/organism='Hepatitis virus (hepatitis C	FT
FT	source	1.15	Location/Qualifiers	
FT	source	1.15	/organism='unidentified'	
FT	source	1.15	/mol_type='genomic RNA'	
FT	source	1.15	/db_xref='taxon:32644'	
ORIGIN				
Query Match	1.8%; Score 11; DB 6; Length 15;			
Best Local Similarity	100.0%; Pred. No. 3.3e+06;			
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	57 CTGGGCTAAG 67			
DB	1 CTGGGCTAAG 11			
RESULT 260				
LOCUS	A66853	16 bp	DNA	linear
DEFINITION	Sequence 20 from Patent W09740193.			PAT 29-MAR-1999
ACCESSION	A66853			
VERSION	A66853.1 GI:4538224			
KEYWORDS	unidentified			
SOURCE	unidentified			
ORGANISM	unclassified			
REFERENCE	1 (bases 1 to 16)			
AUTHORS	Stuyver, L., Kossau, R. and Maertens, G.			
TITLE	METHOD FOR TYPING AND DETECTING HBV			
JOURNAL	Patent: WO 9740193-A 20 30-OCT-1997;			
FEATURES	INNOGENETICS NV (BE)			
source	Location/Qualifiers			
1.16	/organism='unidentified'			
/mol_type='unassigned DNA'				
/db_xref='taxon:32644'				
ORIGIN				
Query Match	1.8%; Score 11; DB 6; Length 16;			
Best Local Similarity	100.0%; Pred. No. 3.3e+06;			
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	437 ACTGCTGAAT 447			
DB	13 ACTGCTGAAT 3			
RESULT 261				
LOCUS	AR089188	16 bp	DNA	linear
DEFINITION	Sequence 4 from patent US 5994056.			PAT 07-SEP-2000
ACCESSION	AR089188			
VERSION	AR089188.1 GI:10015945			
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	unclassified			
REFERENCE	1 (bases 1 to 16)			
AUTHORS	Higuchi, R.G.			
TITLE	Homogeneous methods for nucleic acid amplification and detection			
JOURNAL	Patent: US 5994056-A 4 30-NOV-1999;			
FEATURES	Location/Qualifiers			
source	1.16			
/organism='unknown'				
/mol_type='unassigned DNA'				
ORIGIN				
Query Match	1.8%; Score 11; DB 6; Length 16;			
Best Local Similarity	100.0%; Pred. No. 3.3e+06;			
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

QY 219 CCGCTGCTACC 229
 DB 11 CCGCTGCTACC 1

RESULT 262
 ARI23643/c 16 bp DNA linear PAT 16-MAY-2001
 LOCUS ARI23643
 DEFINITION Sequence 4 from patent US 6171785.
 ACCESSION ARI23643
 VERSION ARI23643.1 GI:14109004
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 16)
 TITLE Higuchi,R.G.
 METHODS Methods and devices for homogeneous nucleic acid amplification and detector

JOURNAL Patent: US 6171785-A 4 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 1.8%; Score 11; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 CCGCTGCTACC 229
 DB 11 CCGCTGCTACC 1

RESULT 263
 I14457 16 bp DNA linear PAT 26-SEP-1995
 LOCUS I14457
 DEFINITION Sequence 31 from patent US 5449768.
 ACCESSION I14457
 VERSION I14457.1 GI:996940
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 16)
 TITLE Chakraborty,P.R., Dashkevicz,M., Eldbrecht,A., Feigheimer,S.D.,
 Liberator,P.A. and Profous-Juchelka,H.
 JOURNAL Eimeria praecox 16S rDNA probes
 PATENT: US 5449768-A 31 12-SEP-1995;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 1.8%; Score 11; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
 DB 3 CGCAGGCTGA 13

RESULT 264
 I27300 16 bp DNA linear PAT 06-FEB-1997
 LOCUS I27300
 DEFINITION Sequence 31 from patent US 5563256.
 ACCESSION I27300
 VERSION I27300.1 GI:1818076
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 152 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 16)
 TITLE Chakraborty,P.R., Dashkevicz,M., Eldbrecht,A., Feigheimer,S.D.,
 Liberator,P.A. and Profous-Juchelka,H.
 JOURNAL Eimeria tenella 16S rDNA probes
 PATENT: US 5563256-A 31 08-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 1.8%; Score 11; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGA 365
 DB 3 CGCAGGCTGA 13

RESULT 265
 I27973 16 bp DNA linear PAT 06-FEB-1997
 LOCUS I27973
 DEFINITION Sequence 145 from patent US 5567809.
 ACCESSION I27973
 VERSION I27973.1 GI:1818749
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 145 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 1.8%; Score 11; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCTGGAGC 255
 DB 1 CCTCTGGAGC 11

RESULT 266
 I27980 16 bp DNA linear PAT 06-FEB-1997
 LOCUS I27980
 DEFINITION Sequence 152 from patent US 5567809.
 ACCESSION I27980
 VERSION I27980.1 GI:1818756
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.
 TITLE Methods and reagents for HLA DRbeta DNA typing
 JOURNAL Patent: US 5567809-A 152 22-OCT-1996;
 FEATURES Location/Qualifiers
 source 1..16
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 1.8%; Score 11; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
|||||
Db 16 CCTCCTGGAGC 6

RESULT 267

LOCUS 127982 16 bp DNA linear PAT 06-FEB-1997

DEFINITION Sequence 154 from patent US 5567809.

ACCESSION 127982

VERSION 127982.1 GI:1818758

KEYWORDS

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 16)

AUTHORS Apple,R.J., Erlich,H.A., Griffith,R.L. and Scharf,S.J.

TITLE Methods and reagents for HLA DRbeta DNA typing

JOURNAL Patent: US 5567809-A 154 22-OCT-1996;

FEATURES

Location/Qualifiers

1..16

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 CCTCCTGGAGC 255
|||||
Db 1 CCTCCTGGAGC 11

RESULT 268

LOCUS BD093179 16 bp DNA linear PAT 27-AUG-2002

DEFINITION A gene coading a cyclic lopopeptide acylase and an expression

thereof.

ACCESSION BD093179

VERSION BD093179.1 GI:22638767

KEYWORDS WO 0102585-A/42.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 16)

AUTHORS Shihata,T., Noguchi,Y. and Ymashita,M.

TITLE A gene coading a cyclic lopopeptide acylase and an expression

Patent: WO 0102585-A 42 11-JAN-2001;

JOURNAL FUJISAWA PHARMACEUTICAL CO LTD,TAKASHI SHIBATA,YUJI NOGUCHI,MICHIO

YMAISHITA

FEATURES

Location/Qualifiers

OS Artificial Sequence

FN WO 0102585-A/42

PD 11-JAN-2001

PF 28-JUN-2000 WO 2000JP004285

PR 02-JUL-1999 JP 99P 189644

PI TAKASHI SHIBATA,YUJI NOGUCHI,MICHIO YMAISHITA

PC C12N15/55,C12N1/21,C12N9/14

CC Oligonucleotide designed to act as sequencing primer. FH Key

Location/Qualifiers

1..16

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GAGACCTACT 86
|||||
Db 4 GAGACCTACT 14

RESULT 269

LOCUS A42338 17 bp DNA linear PAT 05-MAR-1997

DEFINITION Sequence 10 from Patent WO9502057.

ACCESSION A42338

VERSION A42338.1 GI:2297815

KEYWORDS

SOURCE

ORGANISM unidentified

REFERENCE 1 (bases 1 to 17)

AUTHORS Gusterson,B.A., Crompton,M.R., Mitchell,P.J., Barker,K.T.,

Kamatli,T., Page,M.J. and Spence,P.

TITLE PROTEIN TYROSINE KINASE AND LIGANDS THEREOF

JOURNAL Patent: WO 9502057-A 10 19-JAN-1995;

COMMENT CANCER RES INST (GB)

Other publication AU 7080994 950206.

Location/Qualifiers

1..17

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 GCCACGTGGA 174
|||||
Db 4 GCCACGTGGA 14

RESULT 270

LOCUS AR039557 17 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 405 from patent US 5807743.

ACCESSION AR039557

VERSION AR039557

KEYWORDS AR039557.1 GI:5958920

SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Stinchcomb,D.T. and McSwigen,J.A.

TITLE Interleukin-2 receptor gamma-chain ribozymes

JOURNAL Patent: US 5807743-A 405 15-SEP-1998;

Location/Qualifiers

1..17

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 CCTTTGCCCC 547
|||||
Db 6 CCTTTGCCCC 16

RESULT 271

LOCUS AR039559 17 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 407 from patent US 5807743.

ACCESSION AR039559

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.3e+06;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

VERSION AR039559.1 GI:5958922
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 407 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 537 CCTTTGCCCC 547
DB 5 CCTTTGCCCC 15

RESULT 272
LOCUS AR039561 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 409 from patent US 5807743.
ACCESSION AR039561
VERSION AR039561.1 GI:5958924
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T. and McSwiggen,J.A.
TITLE Interleukin-2 receptor gamma-chain ribozymes
JOURNAL Patent: US 5807743-A 409 15-SEP-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 537 CCTTTGCCCC 547
DB 4 CCTTTGCCCC 14

RESULT 273
LOCUS AR057431 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1635 from patent US 5837542.
ACCESSION AR057431
VERSION AR057431.1 GI:5983008
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1635 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
DB 5 TGCTCTTCCTC 15

RESULT 274
LOCUS AR057487 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1691 from patent US 5837542.
ACCESSION AR057487
VERSION AR057487.1 GI:5983064
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1691 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
DB 5 TGCTCTTCCTC 15

RESULT 275
LOCUS AR057566 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1770 from patent US 5837542.
ACCESSION AR057566
VERSION AR057566.1 GI:5983143
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1770 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
DB 3 TGCTCTTCCTC 13

RESULT 276
LOCUS AR057626 17 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1830 from patent US 5837542.
ACCESSION AR057626
VERSION AR057626.1 GI:5983203
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1830 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
5 ACCTCCTGGAG 15

Db

RESULT 277
AR057632 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1836 from patent US 5837542.
DEFINITION AR057632
ACCESSION AR057632.1 GI:5983209
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1836 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
5 ACCTCCTGGAG 15

Db

RESULT 278
AR057687 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1891 from patent US 5837542.
DEFINITION AR057687
ACCESSION AR057687.1 GI:5983264
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1891 17-NOV-1998;
FEATURES Location/Qualifiers

source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
|||||
5 TGCTCTTCCTC 15

Db

RESULT 279
AR057690 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1894 from patent US 5837542.
DEFINITION AR057690
ACCESSION AR057690.1 GI:5983267
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1894 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTC 186
|||||
2 TGCTCTTCCTC 12

Db

RESULT 280
AR057764 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1968 from patent US 5837542.
DEFINITION AR057764
ACCESSION AR057764.1 GI:5983341
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1968 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
5 ACCTCCTGGAG 15

Db

RESULT 281
LOCUS AR057777 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1981 from patent US 5837542.
ACCESSION AR057777
VERSION AR057777.1 GI:5983354
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1981 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
Db 5 TGCTCTTCCTC 15

RESULT 282
LOCUS AR057780 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1984 from patent US 5837542.
ACCESSION AR057780
VERSION AR057780.1 GI:5983357
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1984 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
Db 2 TGCTCTTCCTC 12

RESULT 283
LOCUS AR057782 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1986 from patent US 5837542.
ACCESSION AR057782
VERSION AR057782.1 GI:5983359
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and

TITLE Draper,K.G.
JOURNAL Intercellular adhesion molecule-1 (ICAM-1) ribozymes
FEATURES Patent: US 5837542-A 1986 17-NOV-1998;
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
Db 5 TGCTCTTCCTC 15

RESULT 284
LOCUS AR115189 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1635 from patent US 6132967.
ACCESSION AR115189
VERSION AR115189.1 GI:14095511
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1635 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
Db 5 TGCTCTTCCTC 15

RESULT 285
LOCUS AR115245 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1691 from patent US 6132967.
ACCESSION AR115245
VERSION AR115245.1 GI:14095567
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1691 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 176 TGCTCTTCCTC 186
Db 5 TGCTCTTCCTC 15

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186
|||||
5 TGCTCTTCTC 15

Db 5 TGCTCTTCTC 15

RESULT 286
AR115324
LOCUS AR115324 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1770 from patent US 6132967.
ACCESSION AR115324
VERSION AR115324.1 GI:14095646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1770 17-OCT-2000;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186
|||||
3 TGCTCTTCTC 13

Db 3 TGCTCTTCTC 13

RESULT 287
AR115384
LOCUS AR115384 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1830 from patent US 6132967.
ACCESSION AR115384
VERSION AR115384.1 GI:14095706
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1830 17-OCT-2000;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
5 ACCTCCTGGAG 15

Db 5 ACCTCCTGGAG 15

RESULT 288
AR115390
LOCUS AR115390 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1836 from patent US 6132967.

ACCESSION AR115390
VERSION AR115390.1 GI:14095712
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1836 17-OCT-2000;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAG 254
|||||
5 ACCTCCTGGAG 15

Db 5 ACCTCCTGGAG 15

RESULT 289
AR115445
LOCUS AR115445 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1891 from patent US 6132967.
ACCESSION AR115445
VERSION AR115445.1 GI:14095767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1891 17-OCT-2000;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCTC 186
|||||
5 TGCTCTTCTC 15

Db 5 TGCTCTTCTC 15

RESULT 290
AR115448
LOCUS AR115448 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1894 from patent US 6132967.
ACCESSION AR115448
VERSION AR115448.1 GI:14095770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)

JOURNAL Patent: US 6132967-A 1994 17-OCT-2000;
 FEATURES Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Query Match 1.8%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 176 TGCTCTTCCTC 186
 |||||
 Db 2 TGCTCTTCCTC 12

RESULT 291

AR115522 17 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 1968 from patent US 6132967.
 ACCESSION AR115522
 VERSION AR115522.1 GI:14095844
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
 TITLE Ribozyme treatment of diseases or conditions related to levels of
 JOURNAL intercellular adhesion molecule-1 (ICAM-1)
 FEATURES Patent: US 6132967-A 1994 17-OCT-2000;
 Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 244 ACCTCCTGAG 254
 |||||
 Db 5 ACCTCCTGAG 15

RESULT 292
 AR115535 17 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 1981 from patent US 6132967.
 ACCESSION AR115535
 VERSION AR115535.1 GI:14095857
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
 TITLE Ribozyme treatment of diseases or conditions related to levels of
 JOURNAL intercellular adhesion molecule-1 (ICAM-1)
 FEATURES Patent: US 6132967-A 1994 17-OCT-2000;
 Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 176 TGCTCTTCCTC 186
 |||||
 Db 2 TGCTCTTCCTC 12

Qy 176 TGCTCTTCCTC 186
 |||||
 Db 5 TGCTCTTCCTC 15

RESULT 293

AR115538 17 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 1984 from patent US 6132967.
 ACCESSION AR115538
 VERSION AR115538.1 GI:14095860
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
 TITLE Ribozyme treatment of diseases or conditions related to levels of
 JOURNAL intercellular adhesion molecule-1 (ICAM-1)
 FEATURES Patent: US 6132967-A 1994 17-OCT-2000;
 Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 176 TGCTCTTCCTC 186
 |||||
 Db 2 TGCTCTTCCTC 12

RESULT 294
 AR115540 17 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 1986 from patent US 6132967.
 ACCESSION AR115540
 VERSION AR115540.1 GI:14095862
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
 TITLE Ribozyme treatment of diseases or conditions related to levels of
 JOURNAL intercellular adhesion molecule-1 (ICAM-1)
 FEATURES Patent: US 6132967-A 1994 17-OCT-2000;
 Location/Qualifiers
 source 1..17
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 1.8%; Score 11; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.3e+06;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Qy 176 TGCTCTTCCTC 186
 |||||
 Db 5 TGCTCTTCCTC 15

RESULT 295

AR142556 17 bp DNA linear PAT 08-AUG-2001
 LOCUS
 DEFINITION Sequence 15 from patent US 6203801.
 ACCESSION AR142556
 VERSION AR142556.1 GI:15103842

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 17)
TITLE Unclassified.
JOURNAL Coccidioides polysaccharide and vaccines
PATENT: US 6203801-A 15 20-MAR-2001;
FEATURES Location/Qualifiers
1. 17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 586 TTGGGACTTTG 596
|||||
6 TTGGGACTTTG 16
Db
RESULT 296
AR142558 17 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 17 from patent US 6203801.
ACCESSION AR142558
VERSION AR142558.1 GI:15103844
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polysaccharide and vaccines
JOURNAL Patent: US 6203801-A 17 20-MAR-2001;
FEATURES Location/Qualifiers
1. 17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 586 TTGGGACTTTG 596
|||||
6 TTGGGACTTTG 16
Db
RESULT 297
AR142560 17 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 19 from patent US 6203801.
ACCESSION AR142560
VERSION AR142560.1 GI:15103846
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polysaccharide and vaccines
JOURNAL Patent: US 6203801-A 19 20-MAR-2001;
FEATURES Location/Qualifiers
1. 17
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 1.8%; Score 11; DB 6; Length 17;
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QY 586 TTGGGACTTTG 596
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6 TTGGGACTTTG 16
Db
RESULT 298
AR142562 17 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 21 from patent US 6203801.
ACCESSION AR142562
VERSION AR142562.1 GI:15103848
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polysaccharide and vaccines
JOURNAL Patent: US 6203801-A 21 20-MAR-2001;
FEATURES Location/Qualifiers
1. 17
/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 586 TTGGGACTTTG 596
|||||
6 TTGGGACTTTG 16
Db
RESULT 299
BD254479 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254479
VERSION BD254479.1 GI:33064249
KEYWORDS JP 2002541795-A/2272.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blat,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2272 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2272
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI 12-APR-1999 US 60/129390
PT LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91)
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1. 17
/organism='Eukaryote',
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1. 17
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Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 586 TTGGGACTTTG 596
|||||
6 TTGGGACTTTG 16
Db
RESULT 298
AR142562 17 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 21 from patent US 6203801.
ACCESSION AR142562
VERSION AR142562.1 GI:15103848
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Schaad,T.Cornelis., Kuiper,C.Maria. and Vermeulen,A.Nicolaas.
TITLE Coccidioides polysaccharide and vaccines
JOURNAL Patent: US 6203801-A 21 20-MAR-2001;
FEATURES Location/Qualifiers
1. 17
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 1.8%; Score 11; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 586 TTGGGACTTTG 596
|||||
6 TTGGGACTTTG 16
Db
RESULT 299
BD254479 17 bp DNA linear PAT 17-JUL-2003
LOCUS Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254479
VERSION BD254479.1 GI:33064249
KEYWORDS JP 2002541795-A/2272.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blat,L., Zwick,M., Pavco,P. and Mcswigen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2272 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2272
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PI 12-APR-1999 US 60/129390
PT LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,
PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91)
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1. 17
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Location/Qualifiers
1. 17
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ORIGIN

/mol_type="genomic DNA"
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QY 514 CTCTCCAGACA 524
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Db 7 CTCTCCAGACA 17

RESULT 300

BD254480 17 bp DNA linear PAT 17-JUL-2003
LOCUS BD254480 Regulation of repressor genes using nucleic acid molecules.
DEFINITION
ACCESSION BD254480
VERSION BD254480.1 GI:33064250
KEYWORDS JP 2002541795-A/2273.
SOURCE JP 2002541795-A/2273.
ORGANISM unidentified
unclassified
unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2273 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2273
PD 10-DEC-2002 JP 2000611654
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
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/db_xref="taxon:32644"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e+06;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 514 CTCTCCAGACA 524
|||||
Db 5 CTCTCCAGACA 15

Search completed: March 4, 2004, 22:53:41
Job time : 2790 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 5, 2004, 00:22:13 ; Search time 2507 Seconds

(without alignments)
2358.481 Million cell updates/sec

Title: US-09-966-880A-8

Perfect score: 198
Sequence: 1 MDSLMNRKFLYQKVRW.....ILPLVEVDLRDAFRTGL 198

Scoring table:

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Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Word size: 1

Total number of hits satisfying chosen parameters: 7974

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: listing first 45 summaries

Command line parameters:

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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20
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-NO MAP -LRGB=QUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

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2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_fut:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	2.0	14	12	BM397622
2	4	2.0	14	12	BM398220
3	4	2.0	14	14	CA850755
4	4	2.0	15	13	BQ584986
5	4	2.0	16	9	A1075064
6	4	2.0	16	9	A1188895
7	4	2.0	16	12	BG925060
8	4	2.0	19	9	AA885697
9	4	2.0	19	11	CNS08062
10	4	2.0	19	14	CF305339
11	4	2.0	19	14	CF316655
12	4	2.0	19	14	CF337608
13	4	2.0	19	28	AZ307864
14	4	2.0	19	28	AZ309643
15	4	2.0	19	28	AZ361152
16	4	2.0	19	28	AZ394192
17	4	2.0	19	28	AZ418201
18	4	2.0	19	28	AZ441188
19	4	2.0	19	28	AZ447414
20	4	2.0	19	28	AZ478491
21	4	2.0	19	28	AZ498063
22	4	2.0	19	28	AZ582154
23	4	2.0	19	28	AZ595016
24	4	2.0	19	28	AZ595242
25	4	2.0	19	28	AZ617087
26	4	2.0	19	28	AZ661787
27	4	2.0	19	28	AZ784061
28	4	2.0	19	28	AZ799394
29	4	2.0	19	28	AZ834391
30	4	2.0	19	28	AZ864551
31	4	2.0	20	9	AU013258
32	4	2.0	20	9	AU255876
33	4	2.0	20	13	BX558127
34	4	2.0	20	14	CA851019
35	4	2.0	20	14	CF322764
36	4	2.0	20	14	CF327699
37	4	2.0	20	28	AZ303578
38	4	2.0	20	28	AZ307763
39	4	2.0	20	28	AZ331739
40	4	2.0	20	28	AZ348201
41	4	2.0	20	28	AZ387854
42	4	2.0	20	28	AZ400362
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ALIGNMENTS

RESULT 1	14 bp	mrna	EST 17-JAN-2002
BM397622	5009-0-35	C02.t.2 Chilocat/Turkewitz cDNA (large fraction)	
LOCUS	BM397622	Tetrahymena thermophila cDNA, mRNA sequence.	
DEFINITION	BM397622.1	GI:18197675	
ACCESSION	BM397622	EST.	
VERSION	BM397622.1	Tetrahymena thermophila	
KEYWORDS	EST.	Tetrahymena thermophila	
SOURCE	EST.	Tetrahymena thermophila	
ORGANISM	EST.	Tetrahymena thermophila	
REFERENCE	1	(bases 1 to 14)	

AUTHORS Turkewitz, A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E.,
Frankel, J., and Klobutcher, J.
TITLE EST from *Tetrahymena thermophila*, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3

FEATURES
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/note="Vector: Bluescript2 SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.23e+05 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398220 (1-14)

Cy 120 lysalagluPro 123

DB 2 AAGCTGAGCCA 13

RESULT 2
BM398220/c 14 bp mRNA linear EST 17-JAN-2002
LOCUS 5009-0-42-D11.c.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398220
VERSION BM398220.1 GI:18198273
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 14)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orías, E., Kirk, K.E.,
Frankel, J., and Klobutcher, J.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3

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1. .14
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/mol_type="rRNA"
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/note="Vector: Bluescript2 SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:
Pred. No.: 3.23e+05 Length: 14
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398220 (1-14)

Cy 167 gluAserVal 170
DB 14 GAGAAATAGTGA 3

RESULT 3
CA850755/c 14 bp mRNA linear EST 01-AUG-2003
LOCUS D06B10.B10.04.ab1 cDNA Peking library 2, 4 day SCN3 glycine max
DEFINITION cDNA clone D06B10 5', mRNA sequence.
ACCESSION CA850755
VERSION CA850755.1 GI:33387548
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae;
glycine.
1 (bases 1 to 14)
Alkharouf, N.W., Khan, R., and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
source
1. .14
/organism="Glycine max"
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/cultivar="Peking"
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extracted from Peking roots 2 and 4 days past invasion."

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Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA850755 (1-14)

Cy 41 SerPheSerLeu 44
DB 12 AGTTTAGTCTT 1

RESULT 4
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LOCUS BQ584986 15 bp mRNA linear EST 06-DEC-2002
 DEFINITION BQ11826-024-002-K24-SP6 MP12-ADIS-024-inflorescence Beta vulgaris
 CDNA clone 024-002-K24 5-PRIME, mRNA sequence.
 ACCESSION BQ584986
 VERSION BQ584986.1 GI:26114563
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 15)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehnach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 JOURNAL MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
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 /db_xref="taxon:161934"
 /clone="024-002-K24"
 /tissue_type="inflorescence"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-inflorescence"
 /note="Vector: PCWVSPORE6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinzanlebener Saatgut AG Einbeck, Germany, contact:
 b.schulze@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGCTCG-5prime-CDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.47e+05 Length: 15
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 13 Gaps: 0
 US-09-966-880a-8 (1-198) x BQ584986 (1-15)
 QY 177 ArgArgGleLeu 180
 DB 2 AGAGAGATACTT 13
 RESULT 5
 LOCUS A1075064 16 bp mRNA linear EST 27-AUG-1998
 DEFINITION 061911.X1 NCI CGAP Br-2 Homo sapiens CDNA clone IMAGE:1632356 3'
 similar to TR:Q24348 Q24348 FIBRILARIN 1, mRNA sequence.
 ACCESSION A1075064

VERSION A1075064.1 GI:3399844
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 16)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 www-bio.lnl.gov/bdrrp/image/image.html
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 High quality sequence stop: 1.
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 /clone="IMAGE:1632356"
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 /lab_host="DH10B"
 /clone_lib="NCI CGAP Br-2"
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 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified p773
 vector. This library is the normalized version of
 NCI CGAP Br1.1. Library was constructed by Bento Soares
 and M. Patricia Bonaldo."

ORIGIN
 Alignment Scores:
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 Score: 4.00 Matches: 4
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 9 Gaps: 0
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 QY 180 LeuLeuProLeu 183
 DB 1 CTCCTCCCCCTC 12
 RESULT 6
 LOCUS A1188895 16 bp mRNA linear EST 28-OCT-1998
 DEFINITION gdsb06.x1 Soares fetal heart NDBH19W Homo sapiens CDNA clone
 IMAGE:1731539 3' similar to SM:SN22 HUMAN P51531 POSSIBLE GLOBAL
 TRANSCRIPTION ACTIVATOR SNF2L2 1, mRNA sequence.
 ACCESSION A1188895
 VERSION A1188895.1 GI:3740104
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 This clone is available royalty-free through LINTL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Trace considered overall poor quality
 Insert length: 543 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

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1.16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1731539"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_lung_NDHL19W"
/notes="Organ: heart; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGTGGAGCGCGCATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Patima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NDHL19W."
```

ORIGIN

Alignment Scores:

Pred. No.: 3.72e+05 Length: 16
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A118895 (1-16)

QY 94 ValAlaSpPhe 97
 |||||
 5 GTTGCAGACTTT 16

RESULT 7

BG926060

LOCUS

DEFINITION

HNC23-1-Fl.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

16 bp mRNA linear EST 06-NOV-2001
 HNC23-1-Fl.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

UN2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@sk.com
 Seq primer: T7.
 Location/Qualifiers

FEATURES

source

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1.16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/notes="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI;
Directional"
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ORIGIN

Alignment Scores:

Pred. No.: 3.72e+05 Length: 16
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG926060 (1-16)

QY 59 LeuPheLeu 62
 |||||
 2 CTCTCTCTCT 13

RESULT 8

AA885697

LOCUS

DEFINITION

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp mRNA linear EST 09-JUN-1998
 OJ34401.S1 NCI-CGAP LUS Homo sapiens cDNA clone IMAGE:1500217 3'

similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPPL. [1] ; mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

19 bp mRNA linear EST 09-JUN-1998
 OJ34401.S1 NCI-CGAP LUS Homo sapiens cDNA clone IMAGE:1500217 3'

similar to TR:Q92842 Q92842 HOMOLOG OF YEAST UPPL. [1] ; mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmer-Buck, M.D., Ph.D.
 CNDA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Greg Lennon, Ph.D.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINTL at:
www-bio.lnl.gov/bdip/image/image.html
 Insert length: 691 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers
1. .19

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1500217"
/issue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI CGAP L45"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AA885697 (1-19)

QY 127 ArgArgLeuHis 130

Db 8 AGCGCGTTCAT 19

RESULT 9

LOCUS
CNS08V6Z

19 bp mRNA linear HTC 07-JAN-2003

DEFINITION
Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone FK0AAA4CD05 of strain 6-9 of Anopheles gambiae (African malaria mosquito).ACCESSION
BX029847VERSION
BX029847.1 GI:27603128KEYWORDS
HTCSOURCE
Anopheles gambiae (African malaria mosquito)ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;REFERENCE
1 (bases 1 to 19)

Anopheles.

Genoscope.

AUTHORS
Direct SubmissionJOURNAL
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr

- Web : www.genoscope.cns.fr)

FEATURES
Location/Qualifiers

1. .19
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0AAA4CD05"
/plasmid="pME185-FL"
/note="end : 3-PRIME"

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	11	Gaps:	0

US-09-966-880A-8 (1-198) x CNS08V6Z (1-19)

QY 59 LeuLeuPheLeu 62

Db 1 CTCCTCTTCCT 12

RESULT 10

LOCUS
CF305339

19 bp mRNA linear EST 15-AUG-2003

DEFINITION
CLD1--01-H03.b1 Rice cold treated leaf plasmid cDNA library (CLD1)

Oryza sativa cDNA clone CLD1--01-H03, mRNA sequence.

ACCESSION
CF305339VERSION
CF305339.1 GI:33677100KEYWORDS
EST.SOURCE
Oryza sativaORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE
1 (bases 1 to 19)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm, B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="CLD1--01-H03"
/issue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice cold treated leaf plasmid cDNA library (CLD1)"
/note="Vector: pCR4-TOPO, Site 1: EcoRI; Leaf was incubated at 4 C (360uM/m-2sec-1) for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF305339 (1-19)

QY 36 ArgAspSerAla 39

Db 6 CGGACTTCGCT 17

RESULT 11

LOCUS
CF316655

19 bp mRNA linear EST 15-AUG-2003

DEFINITION
HD--06-A14.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-A14, mRNA sequence.ACCESSION
CF316655VERSION
CF316655.1 GI:33688416KEYWORDS
EST.SOURCE
Oryza sativaORGANISM
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharciodeae; Oryzeae; Oryza.
1 (bases 1 to 19)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Yonsei University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
location/Qualifiers
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-A14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDACL1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF31655 (1-19)

QY 59 Leuleupheleu 62
|||||
1 CTTTATTCCTG 12

RESULT 12
CF337608 19 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--08-C02.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--08-C02, mRNA sequence.
ACCESSION CF337608
VERSION CF337608.1 GI:33823602
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharciodeae; Oryzeae; Oryza.
1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
location/Qualifiers

source

1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--08-C02"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
CDNA library (JMT)"
/note="Vector: PCR4-TOPO, Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF337608 (1-19)

QY 59 Leuleupheleu 62
|||||
14 CTCCTCTTCTT 3

RESULT 13
AZ307864 19 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0010F16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0010F16 F, genomic survey sequence.
ACCESSION AZ307864
VERSION AZ307864.1 GI:10347281
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: F column: 16
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0010F16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

location/Qualifiers

/clone.lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ307864 (1-19)

Qy 125 G1|u|e|A|g|a|g| 128
 |||||
 18 GGCTTACGCCG 7

RESULT 14 19 bp DNA linear GSS 29-SEP-2000
 AZ309643
 LOCUS 1M001623F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M001623 F, genomic survey sequence.

ACCESSION AZ309643
 VERSION AZ309643.1 GI:10350661
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0016 row: B column: 23
 Seq primer: CGTGTAAACGACGCGCAT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ309643 (1-19)

Qy 167 G1|u|a|n|s|e|r|v|a|l 170
 |||||
 15 GAGAACTCTGTG 4

RESULT 15 19 bp DNA linear GSS 02-OCT-2000
 AZ361152
 LOCUS 1M010416R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 DEFINITION clone UUGC1M010416 R, genomic survey sequence.

ACCESSION AZ361152
 VERSION AZ361152.1 GI:10474852
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 1 (bases 1 to 19)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islem,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0104 row: A column: 16
 Seq primer: CACACGAAACGATATGAC
 Class: plasmid ends

FEATURES High quality sequence scrop: 19.
Location/Qualifiers

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M010416"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880a-8 (1-198) x AZ394192 (1-19)

QY 85 SerProCyTYr 88
|||||
DB 4 ACCCATGCTAC 15

RESULT 16

AZ394192 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0157609R Mouse 10kb plasmid U081M library Mus musculus genomic
DEFINITION clone U081M0157609 R, genomic survey sequence.

ACCESSION AZ394192
VERSION AZ394192.1 GI:10509264
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0157 row: G column: 09
Seq primer: CACACAGGAAACGCTATGACC
Clase: plasmid ends
High quality sequence scrop: 19.
Location/Qualifiers

FEATURES

source

1..19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U081M0157609"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1lb="Mouse 10kb plasmid U081M library"
/note="Vector: PMD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880a-8 (1-198) x AZ394192 (1-19)

QY 195 ThrLeuGlyLeu 198
|||||
DB 7 ACCCTGGGCTTA 18

RESULT 17

AZ418201 19 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0194M12F Mouse 10kb plasmid U081M library Mus musculus genomic
DEFINITION clone U081M0194M12 F, genomic survey sequence.

ACCESSION AZ418201
VERSION AZ418201.1 GI:10542214
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0194 row: M column: 12
Seq primer: CGTGTGAAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0194M12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ418201 (1-19)

QY 162 TTPGUGUyLau 165

DB 12 TGGGAGGGATTG 1

RESULT 18
AZ441188 19 bp DNA linear GSS 03-OCT-2000
LOCUS AZ441188/c
DEFINITION IM0232004R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0232004 R, genomic survey sequence.
ACCESSION AZ441188
VERSION AZ441188.1 GI:10565117
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvall, B., Hamil, C., Ismail, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0232 row: O column: 04
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
1..19

FEATURES
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0232004"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
Pred. No.: 4.48e+05 Length: 19
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ441188 (1-19)

QY 60 Leuphelenyrg 63

DB 15 CTGTTTAAAGA 4

RESULT 19
AZ447414 19 bp DNA linear GSS 04-OCT-2000
LOCUS AZ447414/c
DEFINITION IM0244L06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0244L06 R, genomic survey sequence.
ACCESSION AZ447414
VERSION AZ447414.1 GI:10599182
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)
 AUTHORS Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunm@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0244 row: L column: 06
 Seg primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
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 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0244L06"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0
 US-09-966-880A-8 (1-198) x AZ478491 (1-19)
 QY 23 GIYARGARGGLU 26
 |||||
 |||||
 DB 19 GGAAGAGGAG 8
 |||||
 |||||
 RESULT 20
 AZ478491 19 bp DNA linear GSS 04-OCT-2000
 LOCUS AZ478491/c
 DEFINITION IM0298P03R Mouse 10kb plasmid UUC1M library Mus musculus genomic
 clone UUC1M0298P03 R, genomic survey sequence.
 ACCESSION AZ478491
 VERSION AZ478491.1 GI:10637389

KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 REFERENCE
 AUTHORS Dunm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D.,Weiss,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunm@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0238 row: P column: 03
 Seg primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="Genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0298P03"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g1|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0
 US-09-966-880A-8 (1-198) x AZ478491 (1-19)
 QY 27 THTTYTLeuCyS 30
 |||||
 |||||
 DB 15 ACATATTGTGT 4
 |||||
 |||||
 RESULT 21
 AZ498063/c

LOCUS AZ498063 19 bp DNA linear GSS 05-OCT-2000
 DEFINITION 1M033508F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M033508 F, genomic survey sequence.
 ACCESSION AZ498063
 VERSION AZ498063.1 GI:10675575
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0335 row: J column: 08
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M033508"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1[4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Db 15 TCTTACGATA 4
 RESULT 22
 LOCUS AZ582154
 DEFINITION 1M0374C19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0374C19 F, genomic survey sequence.
 ACCESSION AZ582154
 VERSION AZ582154.1 GI:11700755
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 CONTACT: Robert B. Weiss
 UNIVERSITY OF UTAH Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0374 row: C column: 19
 Seq primer: CGTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0374C19"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv, Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
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 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g1[4732114|gb|AF129072.1], a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0
 US-09-966-880a-8 (1-198) x AZ498063 (1-19)
 Oy 105 SerLeuArgIle 108

ORIGIN
 Alignment Scores:
 Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservaive: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0

DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ595016 (1-19)

QY 39 AlarhSerphe 42
 |||||
 8 GCTACTCTCTTT 19

RESULT 23
 AZ595016 19 bp DNA linear GSS 13-DEC-2000
 AZ595016/c
 LOCUS
 DEFINITION IM0407C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0407C15 R, genomic survey sequence.

ACCESSION
 AZ595016
 AZ595016.1 GI:11717206

VERSION
 GSS.

KEYWORDS
 Mus musculus (house mouse)

SOURCE
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weisse, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

REFERENCE
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: C column: 19
 Seq primer: CATTGTAAACGACGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 Location/Qualifiers
 1..19
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0407C15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
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 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (9114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
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 and selected for ampicillin resistance."

Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ595016 (1-19)

QY 162 TTPGLUGLYLeu 165
 |||||
 17 TCGGAGGCGCTG 6

RESULT 24
 AZ595242 19 bp DNA linear GSS 13-DEC-2000
 AZ595242/c
 LOCUS
 DEFINITION IM0407C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0407C15 R, genomic survey sequence.

ACCESSION
 AZ595242
 AZ595242.1 GI:11717432

VERSION
 GSS.

KEYWORDS
 Mus musculus (house mouse)

SOURCE
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weisse, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)

REFERENCE
 CONTACT: Robert B. Weiss
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 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0407 row: C column: 15
 Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 19.

FEATURES
 source
 Location/Qualifiers
 1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0407C15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (9114732114[gb|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ALIGNMENT SCORES:

Prod. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ595242 (1-19)

Qy 32 ValVallyAARG 35
14 GTTGTAACGA 3

RESULT 25
AZ617087/C

LOCUS 19 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0448M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0448M12 F, genomic survey sequence.

ACCESSION AZ617087
VERSION AZ617087.1 GI:11739277

KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0448 row: M column: 12
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0448M12"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF199072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ALIGNMENT SCORES:

Prod. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ617087 (1-19)

Qy 149 AantThPheVal 152
18 AATKCAITTTGTC 7

RESULT 26
AZ661787

LOCUS 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0540I06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0540I06 R, genomic survey sequence.

ACCESSION AZ661787
VERSION AZ661787.1 GI:11798933

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0540 row: I column: 06
Seq primer: CACACGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

source

1. 19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0540I06"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ661787 (1-19)

Qy 69 AppleusAppro 72

Db 6 GATCTGATGCC 17

RESULT 27

AZ784061 19 bp DNA linear GSS 16-FEB-2001

LOCUS

DEFINITION 2M0026M20F Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0026M20 F, genomic survey sequence.

AZ784061.1 GI:12919427

VERSION

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0026 row: M column: 20

Seq primer: CGTGTAAACGACGCGCAGT

Class: plasmid ends

High quality sequence strop: 19.

Location/Qualifiers

1.19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGM0026M20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone_lib="Mouse 10kb plasmid UGCGM library"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ784061 (1-19)

Qy 4 LeuLeuMetAsn 7

Db 15 CTCCTTATGAT 4

RESULT 28

AZ799394 19 bp DNA linear GSS 16-FEB-2001

LOCUS

DEFINITION 2M0056J18R Mouse 10kb plasmid UGCGM library Mus musculus genomic clone UGCGM0056J18 R, genomic survey sequence.

AZ799394.1 GI:12950467

VERSION

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenan,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: J column: 18

Seq primer: CACACAGAAACGCTATGACC

Class: plasmid ends

High quality sequence strop: 19.

Location/Qualifiers

1.19

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCGM0056J18"

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/sex="Male"
/lab host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD42 (g1473214[gbl|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ799394 (1-19)

Qy 91 Alarph:Val 94
 |||||
 16 GCAAGCATGTT 5

RESULT 29
AZ834391

LOCUS 19 bp DNA linear GSS 20-FEB-2001

DEFINITION 2M0117N04F Mouse 10kb plasmid UUGCLM library Mus musculus genomic

ACCESSION AZ834391

VERSION AZ834391.1 GI:13004299

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Euarchyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0117 row: N column: 04
 Seq primer: CGTGTAAACAGACGCCACG
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES
source

1. 19

ORIGIN

Alignment Scores:

Pred. No.:	4.48e+05	Length:	19
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ834391 (1-19)

Qy 107 Argillepethr 110

Db 1 AGGATCTTACC 12

RESULT 30
AZ864551

LOCUS 19 bp DNA linear GSS 21-FEB-2001

DEFINITION 2M0174M1F Mouse 10kb plasmid UUGCLM library Mus musculus genomic

ACCESSION AZ864551

VERSION AZ864551.1 GI:13063965

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Euarchyotia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 19)

REFERENCE

AUTHORS

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0174 row: M column: 11

Seq primer: CGTTGTAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0174M11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUCGIM library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.48e+05 Length: 19
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ864551 (1-19)

Oy 6 MetAenAKGARG 9

Db 2 ATGAATCGCCGC 13

RESULT 31

AU013258 20 bp mRNA linear EST 03-AUG-1998

LOCUS AU013258 Schizosaccharomyces pombe late log phase cDNA

DEFINITION AU013258 Schizosaccharomyces pombe cDNA spc07916, mRNA sequence.

ACCESSION AU013258

VERSION AU013258.1 GI:3368049

KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe

REFERENCE 1 (bases 1 to 20)

AUTHORS Morimyo,M. and Mita,K.

FEATURES

source 1..20

/organism="Schizosaccharomyces pombe"
 /mol_type="mRNA"
 /strain="972"
 /db_xref="taxon:4896"
 /clone="spc07916"
 /sex="h minus"
 /clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AU013258 (1-20)

Oy 3 SerLeuLeuMet 6

Db 2 TCATTACTAATG 13

RESULT 32

AU255876 20 bp mRNA linear EST 25-APR-2002

LOCUS AU255876 3'-directed mouse cDNA library Mus musculus cDNA clone

DEFINITION AU255876 3'-directed mouse cDNA library Mus musculus cDNA clone.

ACCESSION AU255876

VERSION AU255876.1 GI:20319029

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)

AUTHORS Kato,K. and Matoba,R.

TITLE Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished (2002)

CONTACT Kikuya Kato

GRADUATE SCHOOL OF BIOLOGICAL SCIENCES

NARA INSTITUTE OF SCIENCE AND TECHNOLOGY

8916-5 TAKAYAMA, IKOMA, NARA 630-0101, JAPAN

TEL: 81-743-72-5581

FAX: 81-743-72-5589

EMAIL: Kkato@bbs.ais-t-nara.ac.jp, URL: <http://love2.ais-t-nara.ac.jp/BEI/index.html>.

FEATURES

source

1..20
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="BED0006684"
 /tissue_type="brain"
 /clone_lib="3'-directed mouse cDNA library"

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AU255876 (1-20)

Qy 125 GYLeuAargArg 128
Db 14 GGCTTAGAAGA 3

RESULT 33
LOCUS BX558127
DEFINITION BX558127 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans CDNA clone Tse6909.glc, mRNA sequence.

ACCESSION EX558127
VERSION EX558127.1 GI:33429274
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 20)
Lehane, M.J., Aksoy, S., Gibson, W., Kethornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.P., Lehane, S. and Hall, N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)

JOURNAL MEDLINE
PUBMED 22881942
14519198

COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
source All clones with suffix glc are reverse primer reads starting at 5' end of the CDNA all pic reads are from the 3' end.
Location/Qualifiers
1..20
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse6909.glc"
/issue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T. brucei"

ORIGIN

Alignment Scores:
Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BX558127 (1-20)

Qy 73 GYARGCvATyr 76
Db 1 GGAGGTGTAT 12

RESULT 34
LOCUS CA851019
DEFINITION D09C05.E05.05.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
CDNA clone D09C05 5', mRNA sequence.
CA851019
VERSION CA851019.1 GI:33387612

KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max

REFERENCE 1 (bases 1 to 20)
Alkharouf, N.W., Khan, R. and Matthews, B.F. Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)

JOURNAL
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@da.ars.usda.gov.

FEATURES
source Location/Qualifiers
1..20
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D09C05"
/issue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; CDNA clones from mRNA extracted from Peking roots 2 and 4 days past invasion."

ORIGIN

Alignment Scores:
Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA851019 (1-20)

Qy 41 SerPheSerLeu 44
Db 18 TCCCTTCNTTA 7

RESULT 35
LOCUS CF322764/c
DEFINITION HDN--02-A02.g1 OSHDAC1-overexpressing transgenic rice lambda phase CDNA library II (HDN) Oryza sativa CDNA clone HDN--02-A02, mRNA sequence.
ACCESSION CF322764
VERSION CF322764.1 GI:33793762
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 20)
Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers

source

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1. 20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--02-A02"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOL8"
/clone_lib="OSHDACT-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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ORIGIN

Alignment Scores:

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880a-8 (1-198) x CF322764 (1-20)

QY 170 Valargleuser 173
20 GTTAGGTTGAGT 9

Db

RESULT 36
CF327699/c 20 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--02-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--02-E17, mRNA sequence.
ACCESSION CF327699.1 GI:33803647
VERSION
KEYWORDS
SOURCE
ORGANISM

Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriactoidae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nam B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

1. 20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

1. 20
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--02-E17"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880a-8 (1-198) x CF327699 (1-20)

QY 180 LeuleuProleu 183
15 CTCCTCCCCCTC 4

Db

RESULT 37
A2303578/c 20 bp DNA linear GSS 29-SEP-2000
LOCUS IM0003H07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UGCGIM0003H07 F, genomic survey sequence.
ACCESSION A2303578
VERSION A2303578.1 GI:10338956
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0003 row: H column: 07
Seq primer: CGTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

JOURNAL

COMMENT

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0003H07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI:473214|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated

FEATURES

source

with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:	2.02%						
DB:	28						

US-09-966-880A-8 (1-198) x AZ307763 (1-20)

QY 62 LeuArgTyrIle 65
15 CTCAGATATATA 4

RESULT 38

AZ307763 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0010F06F Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0010F06 F, genomic survey sequence.

ACCESSION AZ307763
VERSION AZ307763.1 GI:10347078
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0010 row: F column: 06
Seq primer: CATTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0010F06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
4.73e+05	20	4.00	4	0	0	0	0
Percent Similarity:		100.00%					
Best Local Similarity:		100.00%					
Query Match:	2.02%						
DB:	28						

US-09-966-880A-8 (1-198) x AZ307763 (1-20)

QY 172 LeuSerArgGln 175
20 CTCACAGACAA 9

RESULT 39

AZ311739 20 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0059D21R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0059D21 R, genomic survey sequence.

ACCESSION AZ311739
VERSION AZ311739.1 GI:10394723
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606
FAX: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: D column: 21
Seq primer: CACACAGCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers

FEATURES

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/strain="C57BL/6J"
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/clone="UGCGM0059D21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_id="Mouse 10kb plasmid UGCGM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

"/clone.lib/mouse 10kb plasmid UMGCM library"
/note-Vector: PMW42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMW2 [gll4732114]pb AFI28072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent *E. coli* XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-
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1. 1. 20
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BOULCE

/mol_type="genomic DNA"

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 /db_xref="taxon:10090"
 /clone="UUGC1M0147K24"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x AZ387854 (1-20)

Qy 151 PheValGluAsn 154
 Db 15 TTTGTTGAAAT 4

RESULT 42

AZ400362

LOCUS

DEFINITION 1M0166C1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0166C11 R, genomic survey sequence.

ACCESSION AZ400362.1 GI:10515436

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0166 row: C column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends

FEATURES High quality sequence stop: 20.
 Location/Qualifiers
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 /sex="Male"

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 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x AZ400362 (1-20)

Qy 179 ILeuLeuPro 182
 Db 6 ATTITGTTCCA 17

RESULT 43

AZ408559

LOCUS

DEFINITION 1M0179K14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0179K14 R, genomic survey sequence.

ACCESSION AZ408559.1 GI:10532572

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah Genome Center
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0166 row: C column: 11
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends

Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0179 row: K column: 14

Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

1..20

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/clone_1ib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AZ408555 (1-20)

QY 194 ArgThrLeuGly 197
|||||

DB 7 AGGACACTGGGG 18

RESULT 44

AZ486007

LOCUS

DEFINITION IM0313E17R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0313E17 R, genomic survey sequence.

ACCESSION

AZ486007

VERSION

AZ486007.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

University of Utah Genome Center

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0313 row: E column: 17

Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.

FEATURES

source

Location/Qualifiers

1..20

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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_1ib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:

Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x AZ486007 (1-20)

QY 180 LeuLeuProLeu 183
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DB 4 CTCTGCCCTC 15

RESULT 45

AZ489135

LOCUS

DEFINITION IM0319H15R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0319H15 R, genomic survey sequence.

ACCESSION

AZ489135

VERSION

AZ489135.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0319 row: H column: 15
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
FEATURES Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="UTGCM0319H15"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UTGCM library"
 /note="Vector: PMD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0
 US-09-966-880A-8 (1-198) x AZ489135 (1-20)

QY 97 PheLeuAArgGly 100
 |||||
 |||||
Db 8 TTTCGAGGCGA 19

RESULT 46
 AZ630786 20 bp DNA linear GSS 13-DEC-2000
 LOCUS 1M0484U01R Mouse 10kb plasmid UTGCM library Mus musculus genomic
 DEFINITION clone UTGCM0484U01 R, genomic survey sequence.
 ACCESSION AZ630786
 VERSION AZ630786.1 GI:11752976
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0484 row: J column: 01
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 20.
FEATURES Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UTGCM0484U01"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UTGCM library"
 /note="Vector: PMD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g1[4732114]gb|AF129072.1) a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN
 Alignment Scores:
 Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservatve: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0
 US-09-966-880A-8 (1-198) x AZ630786 (1-20)

QY 186 ValAspAspLeu 189
 |||||
 |||||
Db 5 GTTGATGATCTC 16

RESULT 47
 AZ650507 20 bp DNA linear GSS 14-DEC-2000
 LOCUS 1M0520A16R Mouse 10kb plasmid UTGCM library Mus musculus genomic
 DEFINITION clone UTGCM0520A16 R, genomic survey sequence.
 ACCESSION AZ650507
 VERSION AZ650507.1 GI:11785064

Db 19 CTAATATTCCTG 8

RESULT 49
AZ772787/c
LOCUS
DEFINITION 20 bp DNA linear GSS 16-FEB-2001
1M0583M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0583M24 R, genomic survey sequence.

ACCESSION
AZ772787
VERSION
AZ772787.1 GI:12896465
KEYWORDS
GSS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0583 row: M column: 24
Seq primer: CACACAGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0583M24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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of PMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pied. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0

DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ772787 (1-20)

Qy 60 LeupheLeuArg 63
Db 17 TTAATCTTAAGA 6

RESULT 50
AZ775696
LOCUS
DEFINITION 20 bp DNA linear GSS 16-FEB-2001
2M0008K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0008K09 R, genomic survey sequence.

ACCESSION
AZ775696
VERSION
AZ775696.1 GI:12902501
KEYWORDS
GSS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE
Unpublished (2000)
JOURNAL
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0008 row: K column: 09
Seq primer: CACACAGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0008K09"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapored mouse DNA was annealed to
adapored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pied. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0

Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ775696 (1-20)

Qy 103 AenLusSerLew 106
 Db 2 AATCTATCTTA 13

RESULT 51
 AZ776071 20 bp DNA linear GSS 16-FEB-2001
 LOCUS AZ776071/c
 DEFINITION 2M0009124F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0009124 F, genomic survey sequence.

ACCESSION
 AZ776071
 VERSION
 AZ776071.1 GI:12903267
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0009 row: 1 column: 24
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1. 20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0009124"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD29; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 sheared DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|473214|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into

ORIGIN
 Alignment Scores:
 Pred. No.: 4.73e+05 Length: 20
 Score: 4.00 Matches: 4
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.02% Indels: 0
 DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ776071 (1-20)

Qy 126 LeuArgArgLew 129
 Db 14 CTTGGAAGCTTA 3

RESULT 52
 AZ810573 20 bp DNA linear GSS 20-FEB-2001
 LOCUS AZ810573
 DEFINITION 2M0076K11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0076K11 F, genomic survey sequence.

ACCESSION
 AZ810573
 VERSION
 AZ810573.1 GI:12977957
 KEYWORDS
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 20)
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von
 Niederhausern,A. and Wright,D., Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL
 Unpublished (2000)
 COMMENT
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0076 row: K column: 11
 Seq primer: CGTTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 20.
 Location/Qualifiers
 1. 20
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0076K11"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD29; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 sheared DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

ORIGIN

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Alignment Scores:

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ810573 (1-20)

QY 6 MetAmpArg 9

DB 1 ATGAATCGCCG 12

RESULT 53

AZ832946

LOCUS

DEFINITION 2M0113M1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ832946

VERSION AZ832946.1 GI:13002854

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

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COMMENT

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JOURNAL

COMMENT

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ORIGIN

Pred. No.:	4.73e+05	Length:	20
Score:	4.00	Matches:	4
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.02%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x AZ832946 (1-20)

QY 102 ProAmpLeuSer 105

DB 2 CCTAACCTCTCT 13

RESULT 54

AZ834080

LOCUS

DEFINITION 2M0116A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

AZ834080

VERSION AZ834080.1 GI:13003988

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

COMMENT

JOURNAL

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JOURNAL

COMMENT

High quality sequence strop: 20.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0116A09"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ834080 (1-20)

QY 59 LeuLeuPheLeu 62
|||||
5 TTGCTCTTCTA 16

RESULT 55
AZ949545 20 bp DNA linear GSS 27-APR-2001
LOCUS 2M0213E19F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0213E19 F, genomic survey sequence.
ACCESSION AZ949545
VERSION AZ949545.1 GI:13820772
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muride; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 306, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0213 row: E column: 19
Seq primer: CGTGTAAACGACGCGCGT
Class: Plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1..20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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FEATURES

source
1..20
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0213E19"

/sex="Female"
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/clone_1b="Mouse 10kb plasmid UUGC2M library"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Alignment Scores:
Pred. No.: 4.73e+05 Length: 20
Score: 4.00 Matches: 4
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.02% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AZ949545 (1-20)

QY 172 LeuSerArgGln 175
|||||
9 CTCTCTAGACAG 20

RESULT 56
CA853358 9 bp mRNA linear EST 01-AUG-2003
LOCUS B07D03.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
DEFINITION B07D03 5', mRNA sequence.
ACCESSION CA853358
VERSION CA853358.1 GI:33390151
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE 1 (bases 1 to 9)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
JOURNAL Unpublished (2002)
COMMENT Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..9
/organism="Glycine max"
/mol_type="mRNA"
/culturvar="Peking"
/db_xref="taxon:3847"
/clone="B07D03"
/issue_type="Roots"

FEATURES

source
1..9
/organism="Glycine max"
/mol_type="mRNA"
/culturvar="Peking"
/db_xref="taxon:3847"
/clone="B07D03"
/issue_type="Roots"

ORIGIN

/dev_stage="Seedlings"
/clone_lib="CDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."

Alignment Scores:

Pred. No.: 5.5e+07 Length: 9
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA853358 (1-9)

QY 40 Therserpe 42

DB 9 ACNAGCTTT 1

RESULT 57

HSN004456/c standard; mRNA; EST; 10 BP.

AC AL039980;

XX AL039980.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434J1012_r1 (from clone DKFZp434J1012)

DE EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA

CC No. 81 sequence available of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..10

FT /db_xref="taxon:9606"

FT /mol_type="mRNA"

FT /organism="Homo sapiens"

FT /clone_lib="434 (synonym: hnes3). Vector pSport1; host

FT DH10B; sites NotI + SalI

FT /dev_stage="adult"

FT /tissue_type="testis"

XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 other;

Alignment Scores:

Pred. No.: 2.07e+06 Length: 10

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSN004456 (1-10)

QY 193 Pharyng 195

DB 9 TTCGGAGCC 1

RESULT 58

HSN005384/c standard; mRNA; EST; 10 BP.

AC AL040908;

XX AL040908.1

DT 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434J1415_g1 (from clone DKFZp434J1415)

DE EST; expressed sequence tag.

XX Homo sapiens (human)

OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;

OC Eutheria; Primates; Catarrhini; Homiidae; Homo.

XX [1]

RA Bloecher H., Boecher M., Brandt P., Mewes W., Gassenhuber J., Wiemann S.;

RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by GBF within the CDNA

CC No. 81 sequence available of the German Genome Project

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

FT source 1..10

FT /db_xref="taxon:9606"

FT /mol_type="mRNA"

FT /organism="Homo sapiens"

FT /clone_lib="434 (synonym: hnes3). Vector pSport1; host

FT DH10B; sites NotI + SalI

FT /dev_stage="adult"

FT /tissue_type="testis"

XX Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 other;

Alignment Scores:

Pred. No.: 2.07e+06 Length: 10

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Query Match: 1.52% Indels: 0

DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSN005384 (1-10)

QY 105 Serleung 107

DB 10 AGCTTAGCT 2

RESULT 59

CF313993/c

LOCUS CF313993 10 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--02-F15.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--02-F15, mRNA sequence.
 ACCESSION CF313993
 VERSION CF313993.1 GI:33685754
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source location/Qualifiers
 1..10
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HD--02-F15"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
 /note="Vector: PCR4-TOPO, site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.07e+06 Length: 10
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x CF313993 (1-10)
 QY 23 GYARGARG 25
 Db 10 GGCCGAGCG 2
 RESULT 60
 CF323895 10 bp mRNA linear EST 18-AUG-2003
 LOCUS CF323895
 DEFINITION HDN--05-A22.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--05-A22, mRNA sequence.
 ACCESSION CF323895
 VERSION CF323895.1 GI:33796055
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source location/Qualifiers
 1..10
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="HDN--05-A22"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli SOLR"
 /clone_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"
 /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.07e+06 Length: 10
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x CF323895 (1-10)
 QY 123 PROGLUGLY 125
 Db 2 CCCGAGCGC 10
 RESULT 61
 CF339022 10 bp mRNA linear EST 18-AUG-2003
 LOCUS CF339022/c
 DEFINITION RCL1--03-117.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--03-117, mRNA sequence.
 ACCESSION CF339022
 VERSION CF339022.1 GI:33826427
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 10)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 321 6355
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 FEATURES
 source location/Qualifiers
 1..10
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"

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/clone="RC11-03-117"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/notes="Vector: pBluescript SK(+); Site 1: SacI; Site 2: XhoI. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SacI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

```

ORIGIN

Alignment Scores:

Pred. No.:	2.07e+06	Length:	10
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880a-8 (1-198) x CF339022 (1-10)

Oy 43 SerLeuAEP 45
 Db 10 TTCCTAGAT 2

RESULT 62

HSN008167/c
 ID HSN008167 standard; mRNA; EST; 11 BP.

XX AL043317;
 XX SV AL043317.1
 XX DT 12-MAR-1999 (Rel. 59, Created)
 XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 DE Homo sapiens mRNA; EST DKFZp434N0723_r1 (from clone DKFZp434N0723)
 XX EST: expressed sequence tag.
 XX OS Homo sapiens (human)
 XX OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

[1]

RP 1-11
 RA Blum H., Bauersachs S., Mewes W., Gaassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Kiopterapitz 18a D-82152 Martinsried, GERMANY

CC Clone from S. Wiemann, sequenced by LMU within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

Key Location/Qualifiers

FT source 1.11
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone_lib="DKFZp434N0723"
 FT /clone_lib="434 (synonym: htes3). Vector pSPORT1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 SQ Sequence 11 BP; 2 A; 2 C; 4 G; 3 T; 0 other;

Alignment Scores:

Pred. No.:	2.29e+06	Length:	11
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	2	Gaps:	0

US-09-966-880a-8 (1-198) x HSN008167 (1-11)

Oy 193 PhexgThr 195
 Db 9 TTCGGATC 1

RESULT 63

BSG96271 11 bp mRNA linear EST 06-NOV-2001
 BSG96271 HOA28-1-G6 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,
 LOCUS mRNA sequence.
 DEFINITION
 ACCESSION BSG96271 GI:14306512
 VERSION BSG96271.1
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE

AUTHORS Kumar,S., Connor,J.R., Dodde,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sachse,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M., and
 Lark,M.W.
 IDENTIFICATION and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 OSTEOPATHR. CARTIL. 9 (7), 641-653 (2001)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@gsk.com
 Seq primer: T7

FEATURES

Source

1.11
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HOA (Human Osteoarthritic Cartilage)"
 /note="Vector: pSPORT I; Site 1: SalI; Site 2: NotI;
 Directional"

ORIGIN

Alignment Scores:

Pred. No.:	2.29e+06	Length:	11
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880a-8 (1-198) x BSG96271 (1-11)

Oy 111 AlaxgLeu 113
 Db 3 GCCGAGCTC 11

RESULT 64

BSG927412/c

LOCUS BG927412 11 bp mRNA linear EST 06-NOV-2001
 DEFINITION HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 ACCESSION BG927412
 VERSION BG927412.1 GI:14321935
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 11)
 REFERENCE Kumar,S., Connor,J.R., Dadds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathie,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Latk,M.W.
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 JOURNAL MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay_kumar-1@sk.com
 Seq primer: T7.
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1, Site_1: SalI; Site_2: NotI; Directional"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.29e+06 Length: 11
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0
 US-09-966-880a-8 (1-198) x BG927412 (1-11)
 QY 132 AAGAGYVal 134
 |||||
 10 GCTGGCGTA 2
 RESULT 65
 BM395226 11 bp mRNA linear EST 17-JAN-2002
 LOCUS BM395226/c
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM395226
 VERSION BM395226.1 GI:18195279
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 11)
 REFERENCE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 JOURNAL Contact: Turkewitz AP
 COMMENT Molecular Genetics and Cell Biology

University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.29e+06 Length: 11
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0
 US-09-966-880a-8 (1-198) x BM395226 (1-11)
 QY 38 SerAlaThr 40
 |||||
 10 AGCGCCACA 2
 RESULT 66
 BM395984 11 bp mRNA linear EST 17-JAN-2002
 LOCUS BM395984/c
 DEFINITION 5009-0-15-C03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM395984
 VERSION BM395984.1 GI:18196037
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 11)
 REFERENCE Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 JOURNAL Contact: Turkewitz AP
 COMMENT Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 FEATURES
 source Location/Qualifiers
 1..11
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.29e+06 Length: 11
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM3595984 (1-11)

Qy 39 SerAlaThr 40
 DB 11 TCCTGCACC 3

RESULT 67
 BQ587100

LOCUS BQ587100 11 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012350-024-011-122-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
 024-011-122 5-PRIME, mRNA sequence.

ACCESSION BQ587100.1 GI:26116682

VERSION EST.

KEYWORDS Beta vulgaris

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
 Plate: 11 row: 1 column: 22
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1..11

FEATURES

source

/organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KMS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:195759"
 /db_xref="taxon:161934"
 /clone="024-011-122"
 /tissue_type="leaf"
 /lab_host="EMDH108"
 /clone_lib="MP12-ADIS-024-leaf"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener SaatZucht AG Einbeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.tzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.29e+06 Length: 11
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ587100 (1-11)

Qy 181 LeuProLeu 183

DB 2 TTACCTTG 10

RESULT 68
 BQ595495

LOCUS BQ595495 11 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012691-024-022-014-SP6 MP12-ADIS-024-developing root Beta vulgaris
 cDNA clone 024-022-014 5-PRIME, mRNA sequence.

ACCESSION BQ595495

VERSION BQ595495.1 GI:26125078

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 11)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 11 Std Error: 0.00
 Plate: 22 row: 0 column: 14
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1..11

FEATURES

source

/organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KMS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:191359"
 /db_xref="taxon:161934"
 /clone="024-022-014"
 /tissue_type="developing root"
 /lab_host="EMDH108"
 /clone_lib="MP12-ADIS-024-developing root"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener SaatZucht AG Einbeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.tzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.29e+06 Length: 11
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ595495 (1-11)

Qy 181 LeuProLeu 183

|||||

Db 1 CTCCTCTT 9

RESULT 69
CF339065/c 11 bp mRNA linear EST 18-AUG-2003

LOCUS RC11--03-K22.g1 Regenerated callus lambda phage cDNA library (RC11)

DEFINITION Oryza sativa cDNA clone RC11--03-K22, mRNA sequence.

ACCESSION CF339065

VERSION CF339065.1 GI:33826512

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 11)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H. Large-scale Sequencing Analysis of Rice ESTs unpublished (2003)

TITLE Contact: Nam B.H.

AUTHORS Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

JOURNAL Yongin, Kyonggi, Korea

COMMENT Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source location/Qualifiers
1..11
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RC11--03-K22"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RC11)"
/note="Vector: pBluescript SK(+); Site 1: SacI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SetI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

ORIGIN

Alignment Scores:
Pred. No.: 2.29e+06 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF339065 (1-11)

Qy 38 SerIatnr 40
|||||
10 AGTGCACCC 2

RESULT 70
CF543159 11 bp mRNA linear EST 22-SEP-2003

LOCUS S014678-024-030-006-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

DEFINITION 024-030-006 5-PRIME, mRNA sequence.

ACCESSION CF543159

VERSION CF543159.1 GI:34891599

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 11)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U. Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)

JOURNAL 22362189

MEDLINE 12472698

PUBMED

COMMENT Contact: Weishaar B.
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert length: 11 Std Error: 0.00
Plate: 30 row: 0 column: 06
Seq primer: SP6.

FEATURES
source location/Qualifiers
1..11
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936619"
/db_xref="taxon:161934"
/clone="024-030-006"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzlebener Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCTCCG-Sp1-CC-NotI-77; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 2.29e+06 Length: 11
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF543159 (1-11)

Qy 149 AaTnrPhe 151
|||||
1 AACACTTTC 9

RESULT 71
BH129987 11 bp DNA linear GSS 23-JUL-2001

LOCUS G-663.f Maize Random Small-insert Genomic Library Zea mays genomic

DEFINITION clone G-663 both, genomic survey sequence.

ACCESSION BH129987

VERSION BH129987.1 GI:14998894

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 11)
Weyers,B.C., Tingey,S.V. and Morgante,M. Abundance, distribution and transcriptional activity of repetitive elements in the maize genome

JOURNAL
MEDLINE
PUBMED
COMMENT

Genome Res. 11 (10), 1660-1676 (2001)
21475670
11591643
Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com

Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.

Seq primer: M3unitv

Class: shotgun.

FEATURES
source

Location/Qualifiers
1..11
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-663"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="young leaf"
/dev_stage="seedling"
/clone_lib="Maize Random Small-insert Genomic Library"
/note="Vector: PCR-Script; Total genomic DNA was
nebulized; ends were polished with Pfu polymerase and the
fragments cloned into PCR-Script."

ORIGIN

Alignment Scores:

Pred. No.:	2.29e+06	Length:	11
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x BH129987 (1-11)

Qy 195 ThrLeuGly 197

Db 2 ACCCTCGGA 10

RESULT 72
BH129987/c 11 bp DNA linear GSS 23-JUL-2001
BH129987/c 11 bp DNA linear GSS 23-JUL-2001

DEFINITION
G-663.F Maize Random Small-insert Genomic Library Zea mays genomic
clone G-663 both, genomic survey sequence.

ACCESSION
BH129987
BH129987.1 GI:14998894

KEYWORDS
GSS

SOURCE
Zea mays

ORGANISM
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

1 (bases 1 to 11)
Meyers,B.C., Tingey,S.V. and Morgante,M.
Abundance, distribution and transcriptional activity of repetitive
elements in the maize genome

Genome Res. 11 (10), 1660-1676 (2001)

JOURNAL
MEDLINE
PUBMED

COMMENT

Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com

Sequences were trimmed to include only high quality bases; forward and reverse reads were assembled when significant overlaps were detected.

Seq primer: M3unitv

Class: shotgun.

FEATURES

source

Location/Qualifiers
1..11
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="young leaf"
/dev_stage="seedling"
/clone_lib="Maize Random Small-insert Genomic Library"
/note="Vector: PCR-Script; Total genomic DNA was
nebulized; ends were polished with Pfu polymerase and the
fragments cloned into PCR-Script."

ORIGIN

Alignment Scores:

Pred. No.:	2.29e+06	Length:	11
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	28	Gaps:	0

US-09-966-880A-8 (1-198) x BH129987 (1-11)

Qy 98 LeuArgGly 100

Db 11 CTCCTGAGG 3

RESULT 73
HSM007936/c standard; mRNA; EST; 12 BP.
HSM007936 standard; mRNA; EST; 12 BP.

AC AL043086;

SV AL043086.1

XX 12-MAR-1999 (Rel. 59, Created)

DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

XX Homo sapiens mRNA; EST DKFZp434B0723_r1 (from clone DKFZp434B0723)

XX EST; expressed sequence tag.

XX Homo sapiens (human)

XX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.

XX [1]
RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

RL MIPs, Am Klopferpitz 18a D-82152 Martinsried, GERMANY

XX Clone from S. Wiemann, sequenced by LMU within the CDNA

XX No st sequence available

CC This clone is available at the RZPD in Berlin

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

source 1..12
FT /db_xref="taxon:9606"

```

FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_id="434B0723"
FT      /clone_lib="434 (synonym: htes3). Vector pSPORT1, host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 12 bp; 2 A; 3 C; 4 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:      2.51e+06      Length:      12
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             2            Gaps:         0

US-09-966-880A-8 (1-198) x HSM007936 (1-12)

QY      193 Pheargthr 195
Db      10 TTCGGACC 2

RESULT 74
LOCUS   BG925521      12 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
ACCESSION BG925521
VERSION   BG925521.1 GI:14320044
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 12)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,M., Van Horn,M., Mao,J.,
Sathe,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
JOURNAL   21482651
MEDLINE   11597177
PUBMED
COMMENT   Contact: Sanjay Kumar
          UW2109
          GlaxoSmithKline
          709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
          Tel: 610-270-7245
          Fax: 610-270-5598
          Email: sanjay.kumar-1@gsk.com
          Seq primer: 17.
          Location/Qualifiers
            source
              1..12
                /organism="Homo sapiens"
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                /db_xref="taxon:9606"
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                /lab_host="E.coli DH10 B"
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                /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
                Directional"

ORIGIN
Alignment Scores:
Pred. No.:      2.51e+06      Length:      12
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             12            Gaps:         0

US-09-966-880A-8 (1-198) x HSM007936 (1-12)

```

```

US-09-966-880A-8 (1-198) x BG925521 (1-12)

QY      181 LeuProLeu 183
Db      3 CTCCCTC 11

RESULT 75
LOCUS   BQ587766      12 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION B012340-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
          024-010-M01 5-PRIME, mRNA sequence.
ACCESSION BQ587766
VERSION   BQ587766.1 GI:26117348
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amarantaceae; Beta.
1 (bases 1 to 12)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radloff,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL   22362189
MEDLINE   12472698
PUBMED
COMMENT   Contact: Weishaar B
          ADIS DNA core facility at MP1Z
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weishaar@mpiz-koeln.mpg.de
          Insert length: 12 Std Error: 0.00
          Place: 10 row: 10 column: 01
          Seq primer: SP6; CATACGATTATGTGACACTATAG.
          Location/Qualifiers
            1..12
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              /db_xref="GABI:185095"
              /db_xref="taxon:161934"
              /clone="024-010-M01"
              /tissue_type="leaf"
              /lab_host="EMDH10B"
              /clone_lib="MP1Z-ADIS-024-leaf"
              /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinfalteneber Saatzucht AG Rimbach, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-SalI-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-3'; Note:
              Sequencing granted in the context of the GABI-Beet
              Project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung, Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.:      2.51e+06      Length:      12
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             13            Gaps:         0

US-09-966-880A-8 (1-198) x BQ587766 (1-12)

```

QY 3 SerLeuLeu 5

DB 2 TCTCTCTC 10

RESULT 76
LOCUS BQ587766/c 12 bp mRNA linear EST 06-DEC-2002
DEFINITION B01340-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ587766
VERSION BQ587766.1 GI:26117348
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruuck, W., Menze, A., O'Brien, J., Lehnach, H. and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant U. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698

COMMENT
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mplz-koeln.mpg.de
Insert length: 12 Std Error: 0.00
Plate: 10 row: M column: 01
Seq primer: SP6: CATGCACTTACGGTACACTATG.
Location/Qualifiers
1..12
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:185095"
/db_xref="taxon:161934"
/clone="024-010-M01"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: PCMVSPORT6; Site_1: SalI; Site_2: NotI; cDNA library from sugar beet, library provided by KWS Kleinzelleneher Saatnucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-7'; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:
Pred. No.: 2.51e+06 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ587766 (1-12)

QY 24 ArgArgGlu 26
|||||
|
Db 9 AGGAGAG 1

RESULT 77

BQ750930
LOCUS BQ750930 12 bp mRNA linear EST 18-JUL-2002
DEFINITION EST631493 DSCT Colletotrichum trifolii cDNA clone pDSCT1-51, mRNA sequence.
ACCESSION BQ750930
VERSION BQ750930.1 GI:21906335
KEYWORDS EST
SOURCE Colletotrichum trifolii
ORGANISM Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; mitosporic Phyllachoraceae; Colletotrichum.

REFERENCE
AUTHORS Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Chung, F., and Fraser, C.M.
TITLE ESTs from mycelia of Colletotrichum trifolii race 1
JOURNAL Unpublished (2002)
COMMENT Other ESTs: EST631492
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
TIGR sequence name: MTSAB51rv More information is available at: www.medicago.org
Seq primer: (gpa ABA CGA CTC ACT ABA ggg C).
Location/Qualifiers
1..12
/organism="Colletotrichum trifolii"
/mol_type="mRNA"
/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCT1-51"
/tissue_type="mycelia"
/dev_stage="young, actively growing mycelia (3 days after inoculation) grown in liquid culture (curtin minimal medium containing 2% glucose)."
/lab_host="DH5alpha"
/clone_lib="DSCT"
/note="Vector: pBluescript SK+, Site_1: EcoRI; Site_2: EcoRI; isolate: 2sp2; cDNA was prepared from polyA+ enriched RNA. The cDNA was ligated into lambda gfil from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN

Alignment Scores:
Pred. No.: 2.51e+06 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ750930 (1-12)

QY 119 ArgLysAla 121
|||||
|
Db 4 CGAAGGCC 12

RESULT 78
LOCUS BQ750930/c 12 bp mRNA linear EST 18-JUL-2002
DEFINITION EST631493 DSCT Colletotrichum trifolii cDNA clone pDSCT1-51, mRNA sequence.

ACCESSION BQ750930
 VERSION BQ750930.1 GI:21906335
 KEYWORDS EST
 SOURCE Colletotrichum trifolii
 ORGANISM Colletotrichum trifolii
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllochorales; Phyllochoraceae; Mitosporic Phyllochoraceae; Colletotrichum.
 1 (bases 1 to 12)
 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Uteback,T.,
 Cheung,F. and Fraser,C.M.
 ESTs from mycelia of Colletotrichum trifolii race 1
 Unpublished (2002)
 Other ESTs: EST631492
 Contact: Deborah A. Samac
 Department of Plant Pathology
 University of Minnesota
 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
 Tel: 612 625 1243
 Fax: 651 649 5058
 Email: debbysepucini.crl.umn.edu
 TIGR sequence name: MTSAS1TV More information is available at:
 www.medicago.org
 Seq primer: (GPA Ata CGA CTC ACT Ata ggg C).
 Location/Qualifiers
 1..12
 /organism="Colletotrichum trifolii"
 /mol_type="rRNA"
 /strain="race 1"
 /db_xref="taxon:5466"
 /clone="pDSC1-51"
 /tissue_type="mycelia"
 /dev_stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
 /lab_host="DH5alpha"
 /clone_lib="DSC1"
 /note="Vector: pBluescript SK+, Site_1: EcoRI, Site_2: EcoRI; Isolate: 2SP2; cDNA was prepared from polyA+ enriched RNA The cDNA was ligated into Lambda gII from Stratagene and packaged using Gigapack packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.51e+06 Length: 12
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0
 US-09-966-880a-8 (1-198) x BQ750930 (1-12)
 QY 192 Alaphetg 194
 Db 11 GCCTTCGT 3
 RESULT 79
 C51419/c 12 bp mRNA linear EST 11-SEP-1997
 LOCUS C51419 Yuj1 Kohara unpublished cDNA Caenorhabditis elegans cDNA
 DEFINITION clone yk195ell 3', mRNA sequence.
 ACCESSION C51419.1 GI:2389176
 VERSION EST.
 KEYWORDS Caenorhabditis elegans
 SOURCE

ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Pelodetinae; Caenorhabditis.
 1 (bases 1 to 12)
 Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A.,
 Sano,M., Miyata,A. and Nishigaki,A.
 Expression map of the C.elegans genome
 Unpublished (1996)
 Contact: Yuj1 Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykoha@lab.nig.ac.jp.
 Location/Qualifiers
 1..12
 /organism="Caenorhabditis elegans"
 /mol_type="rRNA"
 /strain="CB1489 him-8(e1489)"
 /db_xref="taxon:6239"
 /clone="yk195ell"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"
 /clone_lib="Yuj1 Kohara unpublished cDNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.51e+06 Length: 12
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0
 US-09-966-880a-8 (1-198) x C51419 (1-12)
 QY 106 leuargile 108
 Db 12 CTGGCTATA 4
 RESULT 80
 CF300273 12 bp mRNA linear EST 15-AUG-2003
 LOCUS 7LEAF--04-J19.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 DEFINITION sativa cDNA clone 7LEAF--04-J19, mRNA sequence.
 ACCESSION CF300273
 VERSION CF300273.1 GI:33672034
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 12)
 Song,S.I., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Kim,J.S., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnah@gbio.com, bhnah@bio.myongji.ac.kr.
 Location/Qualifiers
 1..12
 /organism="Oryza sativa"
 /mol_type="rRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"

FEATURES
 source

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 113 LeuTYRphe 115

Db 11 TTATATTTT 3

RESULT 81

CF311969 12 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 113 LeuTYRphe 115

Db 11 TTATATTTT 3

RESULT 81

CF311969 12 bp mRNA linear EST 15-AUG-2003

DEFINITION ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 172 LeuSerArg 174

Db 2 CTGTCAACA 10

RESULT 82

CF311969/c 12 bp mRNA linear EST 15-AUG-2003

LOCUS ABF--07-H13.g1 ABF3-overexpressing transgenic rice plasmid cDNA

DEFINITION library (ABF) Oryza sativa cDNA clone ABF--07-H13, mRNA sequence.

ACCESSION CF311969

VERSION CF311969.1 GI:33683730

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .12

Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--07-H13"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: pCR4-TOPO, Site 1: EcoRI; leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

Pred. No.: 2.51e+06 Length: 12

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF311969 (1-12)

QY 36 ArgAspSer 38

Db 9 CGTGACAGC 1

RESULT 83

CF329021/c 12 bp mRNA linear EST 18-AUG-2003

LOCUS NACL--04-D03.g1 Rice callus plasmid cDNA library (NACL) Oryza

DEFINITION sativa cDNA clone NACL--04-D03, mRNA sequence.

ACCESSION CF329021

VERSION CF329021.1 GI:33806279
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..12
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--04-D03"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.51e+06 Length: 12
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF329021 (1-12)

QY 59 LeuLeuPhe 61
 |||||
 12 TTATTATT 4

RESULT 84
 CF331951 12 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--08-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--08-E07, mRNA sequence.
 VERSION CF331951
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source
 1..12
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--08-E07"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.51e+06 Length: 12
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF331951 (1-12)

QY 11 PheLeuTyr 13
 |||||
 12 TTTTATAT 4

RESULT 85
 AQ903019 12 bp DNA linear GSS 09-JAN-2001
 LOCUS GSETC07904 Trypanosoma cruzi random genomic library Trypanosoma
 DEFINITION cruzi genomic clone G35A7, genomic survey sequence.
 VERSION AQ903019
 KEYWORDS GSS.
 SOURCE Trypanosoma cruzi
 ORGANISM Trypanosoma cruzi
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.
 REFERENCE 1 (bases 1 to 12)
 AUTHORS Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
 TITLE A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery
 JOURNAL Genome Res. 10 (12), 1996-2005 (2000)
 MEDLINE 20568489
 PUBMED 11116094
 COMMENT On Jul 21, 2000 this sequence version replaced gi:6478057.
 Contact: Sanchez D.O.
 Instituto de Investigaciones Biologicas (Univ. Nac. de Gral San Martin)
 Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos Aires, Argentina
 Tel: (54-11) 4580/7255/7
 Fax: (54-11) 4752-9639
 Email: dsanchez@ib.unsam.edu.ar
 Seq primer: T7
 Class: Shotgun.
 Location/Qualifiers
 1..12
 /organism="Trypanosoma cruzi"
 /mol_type="genomic DNA"
 /strain="CL-Brener"
 /db_xref="taxon:5693"
 /clone="G35A7"
 /cell_type="epimastigote"
 /clone_lib="Trypanosoma cruzi random genomic library"
 /note="Vector: PBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb range

was gel purified and cloned into the dephosphorylated
HincII site of the vector"

ALIGNMENT SCORES:

Pred. No.: 2.51e+06 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x AQ903019 (1-12)

QY 58 G|U|L|U|L|U| 60
| | | | | | | | | | | | | |
DB 1 GAAC|TTT|TA 9

RESULT 86
BH127723 12 bp DNA linear GSS 23-JUL-2001
LOCUS G-1021.r Maize Random Small-insert Genomic Library Zea mays genomic
DEFINITION clone G-1021 both, genomic survey sequence.
ACCESSION BH127723
VERSION BH127723.1 GI:14995555
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
TITLE 1 (bases 1 to 12)
ABUNDANCE, distribution and transcriptional activity of repetitive
elements in the maize genome

JOURNAL
MEDLINE Genome Res. 11 (10), 1660-1676 (2001)
PUBMED 11591643
COMMENT Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
detected.
Seq primer: M3reverse
Class: Shotgun.

FEATURES

source Location/Qualifiers
1..12
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-1021"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="Young leaf"
/dev_stage="seedling"
/clone_lib="Maize Random Small-insert Genomic Library"
/note="Vector: PCR-Script; Total genomic DNA was
nubilized; ends were polished with Pfu polymerase and the
fragments cloned into PCR-Script."

ORIGIN

Alignment Scores:
Pred. No.: 2.51e+06 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0

DB: 28 Gaps: 0
US-09-966-880A-8 (1-198) x BH127723 (1-12)

QY 36 A|T|G|A|P|S|E|r 38
| | | | | | | | | | | | | |
DB 1 CGGAG|TTC|TA 9

RESULT 87
BH129328 12 bp DNA linear GSS 23-JUL-2001
LOCUS G-5a10.f Maize Random Small-insert Genomic Library Zea mays genomic
DEFINITION clone G-5a10 both, genomic survey sequence.
ACCESSION BH129328
VERSION BH129328.1 GI:14997569
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
TITLE 1 (bases 1 to 12)
ABUNDANCE, distribution and transcriptional activity of repetitive
elements in the maize genome

JOURNAL
MEDLINE Genome Res. 11 (10), 1660-1676 (2001)
PUBMED 11591643
COMMENT Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
detected.
Seq primer: M3univ
Class: Shotgun.

FEATURES

source Location/Qualifiers
1..12
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-5a10"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="Young leaf"
/dev_stage="seedling"
/clone_lib="Maize Random Small-insert Genomic Library"
/note="Vector: PCR-Script; Total genomic DNA was
nubilized; ends were polished with Pfu polymerase and the
fragments cloned into PCR-Script."

ORIGIN

Alignment Scores:
Pred. No.: 2.51e+06 Length: 12
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 28 Gaps: 0

US-09-966-880A-8 (1-198) x BH129328 (1-12)

QY 123 P|R|O|G|U|G|L|Y 125
| | | | | | | | | | | | | |
DB 1 CCGGAG|G|G|C 9

RESULT 88
CG677120/c

LOCUS CG677120 12 bp DNA linear GSS 03-OCT-2003
 DEFINITION tmc0875 tnf Aegilops tauschii genomic clone tnf1C15, genomic
 survey sequence.
 ACCESSION CG677120
 VERSION CG677120.1 GI:37506044
 KEYWORDS GSS.
 SOURCE Aegilops tauschii
 ORGANISM Aegilops tauschii
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Aegilops.
 1 (bases 1 to 12)
 Li, W., Zhang, P., Fellera, J., Friebe, B. and Gill, B.S.
 Sequence composition, organization and evolution of a basic
 Triticeae genome of the grass family
 Unpublished (2003)
 COMMENT
 Contact: Li, W
 Dr. Bikram S. Gill's Lab
 Wheat Genetics Resource Center, Kansas State University
 4024 Throckmorton, Manhattan, KS 66506-5502, USA
 Tel: 785-532-1108
 Fax: 785-532-5692
 Email: wli@ksu.edu
 Seq primer: 17
 Class: sheared ends.
 FEATURES
 source 1..12
 Location/Qualifiers
 /organism="Aegilops tauschii"
 /mol_type="genomic DNA"
 /strain="AL 8/78"
 /db_xref="taxon:37682"
 /clone="tm17C15"
 /tissue_type="leaves"
 /dev_stage="shoot"
 /lab_host="E. coli strain DH5alpha"
 /note="Vector: PCR 4Bunt-TOP, 0.8-1.2 kb methylation
 filtered genomic DNA library"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.51e+06 Length: 12
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 29 Gaps: 0
 US-09-966-880A-8 (1-198) x CG677120 (1-12)
 QY 2 ASPSerLeu 4
 |||||
 Db 9 GATTCGCTTA 1
 |||||
 RESULT 89
 HSM007977/c
 ID HSM007977 standard; mRNA; EST, 13 BP.
 XX
 AC AL043127;
 XX
 XX AL043127.1
 SV
 XX
 XX 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434D2223_r1 (from clone DKFZp434D2223)
 XX
 XX EST; expressed sequence tag.
 XX
 XX Homo sapiens (human)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 XX

RN [1]
 RP 1-13
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RT
 RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferseplatz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH
 FH Key Location/Qualifiers
 FT source 1..13
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone="DKFZp434D2223"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 FT
 SQ Sequence 13 BP; 2 A; 4 C; 4 G; 3 T; 0 other;
 XX
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x HSM007977 (1-13)
 QY 193 PheArgThr 195
 |||||
 Db 11 TTCCGAGCC 3
 |||||
 RESULT 90
 AA918967
 LOCUS AA918967
 DEFINITION AA918967 13 bp mRNA linear EST 10-JUN-1998
 similar to TR:Q65566 Q65566; contains element PTR7 repetitive
 element; mRNA sequence.
 ACCESSION AA918967
 VERSION AA918967.1 GI:3058857
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 13)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Trace considered overall poor quality
 Insert length: 1058 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1536152"
/issue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kids"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
AACTGAGAGATTGCGCGCATATTTTATTTTATTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Alignment Scores:
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA918967 (1-13)

QY 90 CysAlaArg 92
|||||
DB 3 TGTGCGCGT 11

RESULT 91
A1744941/c 13 bp mRNA linear EST 21-JUN-1999
LOCUS t117e03.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2218588 3'
DEFINITION similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION A1744941
VERSION A1744941.1 GI:5113229
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 13)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNM at:
www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2218588"
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/issue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Ov23"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.35 kb. Tumor types include: mixed
Mullerian tumor, papillary serous, clear cell, spindle
cell. All are primary tumors, metastasis positive. Life
Technologies catalog #: 11534-013"
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ORIGIN

Alignment Scores:
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1744941 (1-13)

QY 59 LeuLeuPhe 61
|||||
DB 11 TTGTGTTT 3

RESULT 92
BG926067 13 bp mRNA linear EST 06-NOV-2001
LOCUS HNC23-1-B8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG926067.1 GI:14320590
VERSION BG926067.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 13)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Satche,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Cowen,M. and
Lark,M.W.

Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries

Osteochondr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE
PUBMED 11597177
CONTACT: Sanjay Kumar
UM2109

GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: 17.
Location/Qualifiers

FEATURES

source

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1. 13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="Cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
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ORIGIN

Alignment Scores:
Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG926067 (1-13)

QY 181 Leuproleu 183
 |||||
 1 CTCCTTCTG 9

RESULT 93
 BG927437 13 bp mRNA linear EST 06-NOV-2001
 LOCUS HNC1.1-17.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 DEFINITION BG927437
 ACCESSION BG927437
 VERSION BG927437.1 GI:14321960
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 13)
 Kumar,S., Connor,J.R., Dodde,R.A., Halsey,W., Van Horn,M., Mao,J., Sathie,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M., and Lark,M.W.
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651
 PUBMED 11597177
 COMMENT Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@sk.com
 Seq primer: T7,
 Location/Qualifiers
 1..13
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /issue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

FEATURES
 source

ORIGIN

Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x BG927437 (1-13)

QY 60 Leuproleu 62
 |||||
 1 CTCCTTCTG 9

RESULT 94
 BM395292/c 13 bp mRNA linear EST 17-JAN-2002
 LOCUS BM395292
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM395292
 VERSION BM395292.1 GI:18195345
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 13)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)

JOURNAL COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3,
 Location/Qualifiers
 1..13
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chicoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x BM395292 (1-13)

QY 72 ProGlyArg 74
 |||||
 11 CCAGGGCGT 3

RESULT 95
 BM395672/c 13 bp mRNA linear EST 17-JAN-2002
 LOCUS BM395672
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM395672
 VERSION BM395672.1 GI:18195725
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 13)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)

JOURNAL COMMENT Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3,
 Location/Qualifiers
 1..13
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"

ORIGIN

/clone_1lb="Chicoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chicoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

Alignment Scores:

Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BM395672 (1-13)

QY 77 ArgValThr 79

DB 10 CGCGTGACC 2

RESULT 96

BQ586028 13 bp mRNA linear EST 06-DEC-2002

LOCUS E012394-024-013-F21-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

DEFINITION 024-013-F21 5-PRIME, mRNA sequence.

ACCESSION BQ586028

VERSION BQ586028.1 GI:26115610

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 13 row: F column: 21

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1. 13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultiivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:186838"

/db_xref="taxon:161934"

/clone="024-013-F21"

/tissue_type="leaf"

/lab_host="EMDH108"

/clone_1lb="MP12-ADIS-024-leaf"

/note="Vector: PCWVSFOR6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator;

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.73e+06 Length: 13
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ586028 (1-13)

QY 172 LeuSerArg 174

DB 10 TTATGACAGA 2

RESULT 97

BQ589768

LOCUS BQ589768

DEFINITION BQ589768

ACCESSION BQ589768

VERSION BQ589768.1

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruick, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP12

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 20 row: D column: 03

Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1. 13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultiivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:190356"

/db_xref="taxon:161934"

/clone="024-020-D03"

/tissue_type="storage root"

/lab_host="EMDH108"

/clone_1lb="MP12-ADIS-024-storage root"

/note="Vector: PCWVSFOR6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-SalI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator;

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.73e+06 Length: 13

Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ589768 (1-13)

QY 60 Leuphelen 62
 |||||
 3 CTCTCTTG 11

RESULT 98
 BQ595423

LOCUS BQ595423 13 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012693-024-022-N20-SP6 MP12-ADIS-024-developing root Beta vulgaris
 CDNA clone 024-022-N20 5-PRIME, mRNA sequence.

ACCESSION BQ595423.1 GI:26125006
 VERSION BQ595423.1
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 13)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

TITLE JOURNAL MEDLINE
 PUBMED 22362189
 COMMENT 12472698

CONTACT: Weishaar B

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 13 Std Error: 0.00
 Plate: 22 row: N column: 20
 Seq primer: SP6, CATACGATTAGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source

1. 13
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding
 line)"
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 /db_xref="taxon:161934"
 /clone="024-022-N20"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-developing root"
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeher Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-SPRIME-CDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0

DB: 13 Gaps: 0
 US-09-966-880A-8 (1-198) x BQ595423 (1-13)

QY 167 G148nsr 169
 |||||
 1 GAGGATTC C 9

RESULT 99
 BQ595471

LOCUS BQ595471 13 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012691-024-022-C18-SP6 MP12-ADIS-024-developing root Beta vulgaris
 CDNA clone 024-022-C18 5-PRIME, mRNA sequence.

ACCESSION BQ595471.1 GI:26125054
 VERSION BQ595471.1
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 13)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

TITLE JOURNAL MEDLINE
 PUBMED 22362189
 COMMENT 12472698

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 13 Std Error: 0.00
 Plate: 22 row: C column: 18
 Seq primer: SP6, CATACGATTAGTGACACTATAG.
 Location/Qualifiers

FEATURES
 source

1. 13
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:191389"
 /db_xref="taxon:161934"
 /clone="024-022-C18"
 /tissue_type="developing root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-developing root"
 /note="Vector: PCWSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzlebeher Saatzzucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-Sali-CCACGCGTCG-SPRIME-CDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ595471 (1-13)

Qy 175 GlnLeuArg 177
 |||||
 Db 4 CAACTGAGG 12

RESULT 100
 CA794347
 LOCUS CA794347 13 bp mRNA linear EST 05-DEC-2002
 DEFINITION Cac_BL_1304 Cac_BL (Bean and Leaf from Amelonado type Cacao)
 Theobroma cacao cDNA clone Cac_BL_1304 5', mRNA sequence.
 CA794347
 ACCESSION CA794347.1 GI:26051423
 VERSION EST.
 KEYWORDS Theobroma cacao (cacao)
 SOURCE Theobroma cacao
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
 Theobroma.

REFERENCE
 1 (bases 1 to 13)
 Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
 Retzel,E.R. and Jones,C.A.
 Gene discovery and microarray analysis of cacao (Theobroma cacao
 L.) varieties
 JOURNAL Planta 216 (2), 255-264 (2002)
 MEDLINE 22375596
 PUBMED 12447539
 COMMENT Contact: Jones, Paul
 Masterfoods
 3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
 Tel: +44 1664 416644
 Email: Paul.Jones@eu.affem.com
 Seq primer: 73.

FEATURES
 source Location/Qualifiers
 1..13
 /organism="Theobroma cacao"
 /mol_type="mRNA"
 /strain="Amelonado type"
 /db_xref="taxon:3641"
 /clone="Cac_BL_1304"
 /tissue_type="Mature leaf and mature bean"
 /cell_type="Whole organ"
 /dev_stage="maturity"
 /lab_host="XL-1 Blue MRF"
 /clone_lib="Cac_BL (Bean and Leaf from Amelonado type
 Cacao)"
 /note="Vector: PBK-CMV; Bean and leaf tissue from an
 Amelonado type Cacao tree."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CA794347 (1-13)

Qy 82 ThrSerTrp 84
 |||||
 Db 2 ACGTCTTG 10

RESULT 101
 CF299938
 LOCUS CF299938/c 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF-04-C12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
 sativa cDNA clone 7LEAF-04-C12, mRNA sequence.
 CF299938
 ACCESSION CF299938.1 GI:33677873
 VERSION EST.
 KEYWORDS Oryza sativa
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomic and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..13
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="7LEAF-04-C12"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN
 Alignment Scores:
 Pred. No.: 2.73e+06 Length: 13
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF299938 (1-13)

Qy 113 LeuTyPhe 115
 |||||
 Db 12 TTTATTTT 4

RESULT 102
 CF306112
 LOCUS CF306112/c 13 bp mRNA linear EST 15-AUG-2003
 DEFINITION HDAL-02-L18.g1 OSHDAC1-overexpressing transgenic rice lambda phage
 cDNA library I (HDAL) Oryza sativa cDNA clone HDAL-02-L18, mRNA
 sequence.
 CF306112
 ACCESSION CF306112.1 GI:33677873
 VERSION EST.
 KEYWORDS Oryza sativa
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomic and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source Location/Qualifiers
 1..13

```

/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDA1-02-118"
/tissue_type="callus"
/dev_stage="proliferated callus on 2M6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDA1)"
/notes="vector: pBlueScript SK(+); Site 1: EcoRI; Site 2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

```

ORIGIN

Alignment Scores:

Pred. No.:	2.73e+06	Length:	13
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF306112 (1-13)

QY 38 SerAlaThr 40

Db 10 AGTGCACC 2

RESULT 103

CF543088 13 bp mRNA linear EST 22-SEP-2003
 LOCUS 5014680-024-030-P08-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-030-P08 5-PRIME, mRNA sequence.

ACCESSION CF543088

VERSION CF543088.1

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 13)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,

COMMENT Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

JOURNAL fingerprinting allows access to 25 000 potential sugar beet genes

MEDLINE Plant J. 32 (5), 845-857 (2002)

PUBMED 22362189

COMMENT 12472698

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert length: 13 Std Error: 0.00

Plate: 30 row: P column: 08

Seq primer: SP6.

Location/Qualifiers

1. 13

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db_xref="GABI:936675"

/db_xref="taxon:161934"

/clone="024-030-P08"

/tissue_type="leaf"

/lab_host="EMDH105"

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/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCW50P06; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet. library provided by KWS
Kleinmannleber Saatzucht AG Rahnbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RBPd/GABI-Primary database: http://gabi.rzpd.de"

```

ORIGIN

Alignment Scores:

Pred. No.:	2.73e+06	Length:	13
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF543088 (1-13)

QY 171 ArgLeuSer 173

Db 12 CGCCTCTCA 4

RESULT 104

CF921303 13 bp mRNA linear EST 05-NOV-2003
 LOCUS gmrhw3-07 G12_1 084 Soybean root hair subtracted cDNA library
 DEFINITION gmrhw3 Glycine max cDNA, mRNA sequence.

ACCESSION CF921303

VERSION CF921303.1

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

REFERENCE 1 (bases 1 to 13)

AUTHORS Scheffler,B.E., Hang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.

TITLE Expressed sequence tags from soybean root hair subtractive cDNA

JOURNAL library

COMMENT Unpublished (2003)

Contact: Gary Stacey

University of Missouri

108 Waters Hall, Columbia, MO 65211, USA

Tel: 573-884-4752

Fax: 573-882-0588

Email: stacey@missouri.edu

Single pass sequence

Seq primer: T7

Location/Qualifiers

1. 13

/organism="Glycine max"

/mol_type="mRNA"

/cultivar="Williams 82"

/db_xref="taxon:3847"

/tissue_type="root hairs"

/clone_lib="Soybean root hair subtracted cDNA library

gmrhw3"

/notes="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones

generated from soybean root hair tissue treated with

Bradyrhizobium japonicum for 3 hours."

ORIGIN

Alignment Scores:

Pred. No.:	2.73e+06	Length:	13
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

```

Query Match:      1.52%      Indels:      0
DB:               14         Gaps:         0

US-09-966-880a-8 (1-198) x CF921303 (1-13)

QY               41 SerPheaser 43
DB              13 TCCCTTTCT 5

RESULT 105
BH170808/c      13 bp      DNA      linear      GSS 03-OCT-2001
LOCUS          BH170808      13 bp      DNA      linear      GSS 03-OCT-2001
DEFINITION     SALK_003378 Arabidopsis thaliana TDNA insertion lines Arabidopsis
ACCESSION      BH170808      thaliana genomic clone SALK_003378, genomic survey sequence.
VERSION        BH170808.1   GI:15906490
KEYWORDS       GSS.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots;
Rosids; eurosoids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1. (bases 1 to 13)
AUTHORS        Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
JOURNAL        A Sequence-Indexed Library of Insertion Mutations in the
COMMENT        Arabidopsis Genome
                Unpublished (2001)
                Contact: Joseph R. Ecker
                Salk Institute Genomic Analysis Laboratory (SIGAL)
                The Salk Institute for Biological Studies
                10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                Tel: 858 453 4100 x1752
                Fax: 858 558 6379
                Email: eckersalk.edu
                This is single pass sequence recovered from the left border of
                TDNA.
                Class: TDNA tagged.
FEATURES
  source
    1..13
    location/Qualifiers
      /organism="Arabidopsis thaliana"
      /mol_type="genomic DNA"
      /strain="Columbia 0"
      /db_xref="taxon:3702"
      /clone="SALK_003378"
      /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

ORIGIN
Alignment Scores:
Pred. No.:      2.73e+06      Length:      13
Score:          3.00         Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:        0
DB:             28           Gaps:          0

US-09-966-880a-8 (1-198) x BH170808 (1-13)

QY               129 LeuHISArg 131
DB              13 CTCACCGC 5

RESULT 106
HSM003815/c     standard; mRNA; EST, 14 BP.
ID              HSM003815
XX

AC              AL039339;
SV              AL039339.1
DT              12-MAR-1999 (Rel. 59, Created)
DT              12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE              Homo sapiens mRNA; EST DKFZp434F1810_r1 (from clone DKFZp434F1810)
XX              EST; expressed sequence tag.
XX              Homo sapiens (human)
XX              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX              Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX              [1]
XX              1-14
XX              Dueterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX              Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX              MITS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX              CLONE from S. Wiemann, sequenced by Oligen within the CDNA
XX              sequencing consortium of the German Genome Project
XX              No sl sequence available
XX              This clone is available at the RZPD in Berlin
XX              Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX              Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX              Key
XX              Location/Qualifiers
XX              FT
XX              source
XX              1..14
XX              /db_xref="taxon:9606"
XX              /mol_type="mRNA"
XX              /organism="Homo sapiens"
XX              /clone="DKFZp434F1810"
XX              /clone_lib="434 (synonym: htee3). Vector pSport1; host
XX              DH10B; sites NotI + SalI"
XX              /dev_stage="adult"
XX              /tissue_type="testis"
XX              SQ
XX              Sequence 14 BP; 3 A; 4 C; 4 G; 3 T; 0 other;

Alignment Scores:
Pred. No.:      2.95e+06      Length:      14
Score:          3.00         Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:        0
DB:             2           Gaps:          0

US-09-966-880a-8 (1-198) x HSM003815 (1-14)

QY               193 PheArgThr 195
DB              12 TCCCGGAC 4

RESULT 107
HSM004378/c     standard; mRNA; EST, 14 BP.
ID              HSM004378
XX              AL039902;
XX              AL039902.1
XX              SV
XX              AL039902.1
XX              12-MAR-1999 (Rel. 59, Created)
XX              12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX              Homo sapiens mRNA; EST DKFZp434G2412_r1 (from clone DKFZp434G2412)
XX              EST; expressed sequence tag.
XX              Homo sapiens (human)
XX              OS

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 XX
 RN
 RP 1-14
 RA Duesterhoeft A., Lauber J., Mewes W., Gaesshuber J., Wiemann S.;
 RT
 RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferstr 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 CC
 XX
 FH Key Location/Qualifiers
 FH
 FT source 1. .14
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 FT
 XX
 SQ Sequence 14 BP; 2 A; 5 C; 4 G; 3 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x HSM004378 (1-14)
 Qy 193 PheargThr 195
 Db 10 TTCGGAGCC 2
 RESULT 108 14 bp mRNA linear EST 06-NOV-2001
 BG924475 HNC27-1-D6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 LOCUS
 DEFINITION
 accession EG924475 14 bp mRNA linear EST 06-NOV-2001
 version BG924475.1 GI:14318998
 keywords EST.
 source Homo sapiens (human)
 organism Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 14)
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
 Lark,M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 2148651
 11597177
 Contact: Sanjay Kumar
 UM2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com
 Seq primer: T7.
 Location/Qualifiers
 1. .14
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0
 US-09-966-880A-8 (1-198) x BG924475 (1-14)
 Qy 111 AlargLeu 113
 Db 1 GCCAGACTC 9
 RESULT 109 14 bp mRNA linear EST 17-JAN-2002
 BM399228
 LOCUS
 DEFINITION
 5009-0-55-Cl2.t.2 Chlloact/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 accession BM399228 14 bp mRNA linear EST 17-JAN-2002
 version BM399228.1 GI:18199281
 keywords EST.
 source Tetrahymena thermophila
 organism Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 14)
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
 Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1. .14
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chlloact/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library
 preparation can be found in Chlloact and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Alignment Scores:
 Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM399228 (1-14)

QY 77 ArgvAlthr 79
 |||||
 DB 10 CCGGTGACT 2

RESULT 110
 BQ590387/c

LOCUS BQ590387/c 14 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012840-024-019-G10-SP6 MP12-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-019-G10 5-PRIME, mRNA sequence.

ACCESSION BQ590387
 VERSION BQ590387.1 GI:26119970
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 14)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 19 row: G column: 10
 Seq primer: SP6; CATGAGATTAGTGACACTATAG.
 Location/Qualifiers

FEATURES

source

1..14
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:189736"
 /db_xref="taxon:161934"
 /clone="024-019-G10"
 /issue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCAGCGCTCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ590387 (1-14)

QY 118 AspArgTys 120
 |||||

DB 10 GACAGGAAG 2

RESULT 111
 BQ590450

LOCUS BQ590450 14 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012839-024-019-A07-SP6 MP12-ADIS-024-storage root Beta vulgaris
 CDNA clone 024-019-A07 5-PRIME, mRNA sequence.

ACCESSION BQ590450
 VERSION BQ590450.1 GI:26120033
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 14)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698

COMMENT Contact: Weisshaar B

ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 19 row: A column: 07
 Seq primer: SP6; CATGAGATTAGTGACACTATAG.
 Location/Qualifiers

FEATURES

source

1..14
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:189667"
 /db_xref="taxon:161934"
 /clone="024-019-A07"
 /issue_type="storage root"
 /lab_host="EMDH10B"
 /clone_lib="MP12-ADIS-024-storage root"
 /note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
 SP6-Sali-CCAGCGCTCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ590450 (1-14)

QY 61 PheLeuArg 63
 |||||

DB 4 TTCTGAGG 12
 |||||

RESULT 112
 BQ593541

LOCUS BQ593541 14 bp mRNA linear EST 06-DEC-2002
 DEFINITION S013408-024-026-P02-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 CDNA clone 024-026-P02 5-PRIME, mRNA sequence.
 ACCESSION BQ593541
 VERSION BQ593541.1 GI:261233124
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,M., Menze,A., O'Brien,J., Lehnach,H.
 and Radcliof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant U. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp1z-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 26 row: P column: 02
 Seq primer: SP6; CATACGATTTCAGTGACACTATAG.
 Location/Qualifiers
 1..14
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KMS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:193314"
 /db_xref="taxon:161934"
 /clone="024-026-P02"
 /issue_type="developing root"
 /lab_host="EMDH108"
 /clone_11b="MP1Z-ADIS-024-developing root"
 /note="Vector: PCWVSFOR16; Site_1: Sall; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzleberer Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
 orientation:
 SPE-Sall-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beeet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0
 US-09-966-880A-8 (1-198) x BQ593541 (1-14)

QY 43 SerLeuasp 45
 Db 5 TCTCTGCAC 13

RESULT 113
 LOCUS BQ593808 14 bp mRNA linear EST 06-DEC-2002
 DEFINITION E012763-024-026-007-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
 CDNA clone 024-026-007 5-PRIME, mRNA sequence.
 ACCESSION BQ593808

VERSION BQ593808.1 GI:261233191
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,M., Menze,A., O'Brien,J., Lehnach,H.
 and Radcliof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant U. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MP1Z
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp1z-koeln.mpg.de
 Insert Length: 14 Std Error: 0.00
 Plate: 26 row: O column: 07
 Seq primer: SP6; CATACGATTTCAGTGACACTATAG.
 Location/Qualifiers
 1..14
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultiivar="KMS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:193044"
 /db_xref="taxon:161934"
 /clone="024-026-007"
 /issue_type="developing root"
 /lab_host="EMDH108"
 /clone_11b="MP1Z-ADIS-024-developing root"
 /note="Vector: PCWVSFOR16; Site_1: Sall; Site_2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinfanzleberer Saatgut AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites Sall-NotI, primer sites and
 orientation:
 SPE-Sall-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beeet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0
 US-09-966-880A-8 (1-198) x BQ593808 (1-14)

QY 42 PheSerLeu 44
 Db 6 TTCTCCCTC 14

RESULT 114
 LOCUS CA798290 14 bp mRNA linear EST 05-DEC-2002
 DEFINITION Cac_BL_611 Cac_BL (Bean and leaf from Ameljonardo type Cacao)
 Theobroma cacao cDNA clone Cac_BL_611 5', mRNA sequence.
 ACCESSION CA798290
 VERSION CA798290.1 GI:26055376
 KEYWORDS EST.
 SOURCE Theobroma cacao (cacao)
 ORGANISM Theobroma cacao

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.

REFERENCE
1 (bases 1 to 14)
Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D., Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties
Planta 216 (2), 255-264 (2002)

JOURNAL
MEDLINE
2237596
12447539
Contact: Jones, Paul
Masterfoods
3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
Tel: +44 1664 416644
Email: Paul.Jones@eu.effem.com
Seq primer: T3.

FEATURES
source
1..14
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelonado type"
/db_xref="taxon:3641"
/clone_lib="Cac BL 611"
/tissue_type="Mature leaf and mature bean"
/cell_type="Whole organ"
/dev_stage="maturity"
/lab_host="Xl-1 Blue WRF"
/clone_lib="Cac BL (Bean and leaf from Amelonado type Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an Amelonado type Cacao tree."

ORIGIN
Alignment Scores:
Pred. No.: 2.95e+06 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA798290 (1-14)

Cy 112 ArgLeuTyr 114
|||||
Db 4 CGCCTATAC 12

RESULT 115
CA853334/c
LOCUS
DEFINITION
14 bp mRNA linear EST 01-AUG-2003
B07A06.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
B07A06.5', mRNA sequence.
CA853334
ACCESSION
CA853334
VERSION
CA853334.1 GI:33390127
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Glycine max
Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
1 (bases 1 to 14)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Km 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350, USA

Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.ueda.gov.
Location/Qualifiers

FEATURES
source
1..14
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3647"
/clone_lib="B07A06"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 12hr SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA extracted from roots of soybean cv. Peking 12 hrs after infection by SCN race 3. These are cloned in pBluescript SK- phagemid."

ORIGIN
Alignment Scores:
Pred. No.: 2.95e+06 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA853334 (1-14)

Cy 179 IleLeuLeu 181
|||||
Db 14 ATCTTGCTC 6

RESULT 116
CF278327
LOCUS
DEFINITION
14 bp mRNA linear EST 14-AUG-2003
14FTL--04-D06.b1 Rice etiolated leaf plasmid cDNA library (14FTL)
Oryza sativa cDNA clone 14FTL--04-D06, mRNA sequence.
CF278327
ACCESSION
CF278327.1 GI:33655713
VERSION
CF278327.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone_lib="14FTL--04-D06"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14FTL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	2.95e+06	Length:	14
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF278327 (1-14)

Oy 34 Lythargarg 36

Db 12 AAGCGAGA 4

RESULT 117

CF300543 14 bp mRNA linear EST 15-AUG-2003

LOCUS 7LEAF--05-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--05-B01, mRNA sequence.

ACCESSION CF300543

VERSION CF300543.1 GI:33672304

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

/culturvar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--05-B01"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	2.95e+06	Length:	14
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF300543 (1-14)

Oy 15 Phelysaen 17

Db 13 TTTAAANT 5

RESULT 119

CF306911 14 bp mRNA linear EST 15-AUG-2003

LOCUS HDAL--05-D06.g1 OshDAC1-overexpressing transgenic rice lambda phage

DEFINITION cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--05-D06, mRNA

ACCESSION CF306911

VERSION CF306911.1 GI:33678672

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

LOCUS CF300543 14 bp mRNA linear EST 15-AUG-2003

DEFINITION 7LEAF--05-B01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

ACCESSION CF300543

VERSION CF300543.1 GI:33672304

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES

source

1. .14

/organism="Oryza sativa"

/mol_type="mRNA"

/culturvar="Nackdong"

/db_xref="taxon:4530"

/clone="7LEAF--05-B01"

/tissue_type="leaf"

/dev_stage="7 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	2.95e+06	Length:	14
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF300543 (1-14)

Oy 15 Phelysaen 17

Db 13 TTTAAANT 5

RESULT 119

CF306911 14 bp mRNA linear EST 15-AUG-2003

LOCUS HDAL--05-D06.g1 OshDAC1-overexpressing transgenic rice lambda phage

DEFINITION cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--05-D06, mRNA

ACCESSION CF306911

VERSION CF306911.1 GI:33678672

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

/clone="HDAL-05-D06"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda

phage cDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB: 14

US-09-966-880a-8 (1-198) x CF307189 (1-14)

Ory 194 ArgThrLeu 196

Db 6 AGGACTCTT 14

RESULT 120

CF307189/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

/clone="HDAL-05-P24"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda

phage cDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

rice Histone Deacetylase overexpression line."

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB: 14

US-09-966-880a-8 (1-198) x CF307189 (1-14)

Ory 38 SerAlaThr 40

Db 10 AGTGCACCC 2

RESULT 121

CF307495/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

/clone="HDAL-06-N23"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda

phage cDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

rice Histone Deacetylase overexpression line."

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB: 14

US-09-966-880a-8 (1-198) x CF307189 (1-14)

Ory 38 SerAlaThr 40

Db 10 AGTGCACCC 2

RESULT 121

CF307495/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..14

/organism="Oryza sativa"

/mol_type="mRNA"

/db_xref="taxon:4530"

/clone="HDAL-06-N23"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda

phage cDNA library I (HDAL)"

/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:

XhoI; Callus was treated with ABA(20um) for 1hour. cDNA

was inserted into lambda Uni-ZAP XR vector at 5' end with

EcoRI and 3' end with XhoI site. mRNA was derived from

rice Histone Deacetylase overexpression line."

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.52%
 DB: 14
 Gaps: 0

US-09-966-880A-8 (1-198) x CF328966 (1-14)

QY 38 SerAlaThr 40
 10 AGTGCACC 2

RESULT 122

CF328966 14 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--04-B19, mRNA sequence.

ACCESSION CF328966 GI:33806172
 VERSION CF328966.1
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..14
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--04-B19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF328966 (1-14)

QY 10 LysPheLeu 12
 2 AAATTTTA 10

RESULT 123

CF328966 14 bp mRNA linear EST 18-AUG-2003
 LOCUS NACL--04-B19.g1 Rice callus plasmid cDNA library (NACL) Oryza
 DEFINITION sativa cDNA clone NACL--04-B19, mRNA sequence.

ACCESSION CF328966 GI:33806172
 VERSION CF328966.1

KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
 source location/Qualifiers

1..14
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--04-B19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF328966 (1-14)

QY 15 PheLysAsn 17
 12 TTTAAAT 4

RESULT 124

CF921312 14 bp mRNA linear EST 05-NOV-2003
 LOCUS gmrhwm3-07.H10.1.066 Soybean root hair subtracted cDNA library
 DEFINITION gmrhwm3 Glycine max cDNA, mRNA sequence.

ACCESSION CF921312
 VERSION CF921312.1 GI:38192106
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 14)
 Schaeffler,B.E., Huang,S., Liu,X., Nguyen,H., Duke,M. and Stacey,G.
 Expressed sequence tags from soybean root hair subtractive cDNA
 library

JOURNAL Unpublished (2003)
 COMMENT Contact: Gary Stacey

University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752
 Fax: 573-882-0588
 Email: stacey@missouri.edu

Single pass sequence
Seq primer: T7FEATURES
Location/Qualifiers

source

1. 14
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Williams 82"
/db_xref="taxon:3847"
/tissue_type="root hairs"
/clone_lib="Soybean root hair subtracted cDNA library
gmhRW3"
/note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones
generated from soybean root hair tissue treated with
Bradyrhizobium japonicum for 3 hours."

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF921312 (1-14)

QY 191 AspAlaphe 193

Db 3 GATGCTTC 11

RESULT 125

BH169716 14 bp DNA linear GSS 03-OCT-2001
LOCUS BH169716 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_001788, genomic survey sequence.

ACCESSION BH169716.1 GI:15905091

VERSION BH169716.1

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shim,P., Zimmerman,J. and Ecker,U.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 14

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/cdna_protocols.html

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x BH169716 (1-14)

QY 72 ProGlyArg 74

Db 6 CCGGCGCCGT 14

RESULT 126

BH169716 14 bp DNA linear GSS 03-OCT-2001
LOCUS BH169716 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_001788, genomic survey sequence.

ACCESSION BH169716.1 GI:15905091

VERSION BH169716.1

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,

Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,

Shim,P., Zimmerman,J. and Ecker,U.R.

A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 14

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/cdna_protocols.html

ORIGIN

Alignment Scores:

Pred. No.: 2.95e+06 Length: 14
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 28 Gaps: 0

US-09-966-880a-8 (1-198) x BH169716 (1-14)

```

QY      110 ThrAlaArg 112
DB      14 ACAGCCCGG 6

RESULT 127
ID      HSM003885 standard; mRNA; EST; 15 BP.
XX
XX      AL039409;
XX
XX      AL039409.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434L1010_r1 (from clone DKFZp434L1010)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      RP 1-15
XX      RA Duisterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
XX      RT /
XX      RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MI MIPs, Am Klopferpitz 18a D-82152 Martinsried, GERMANY
XX
XX      CC Clone from S. Wiemann, sequenced by Qiagen within the CDNA
XX      CC sequencing consortium of the German Genome Project
XX      CC s1 sequence also available
XX      CC This clone is available at the RZPD in Berlin
XX      CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH
XX      FT source      1..15
XX      FT              /db_xref="taxon:9606"
XX      FT              /mol_type="mRNA"
XX      FT              /organism="Homo sapiens"
XX      FT              /clone="DKFZp434L1010"
XX      FT              /clone_1b="434 (synonym: htes3). Vector pSport1; host
XX      FT              DH10B; sites NotI + SalI"
XX      FT              /dev_stage="adult"
XX      FT              /tissue_type="testis"
XX
SQ      Sequence 15 BP; 3 A; 4 C; 5 G; 3 T; 0 other;
XX
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    1.52%          Indels:      0
DB:            2            Gaps:        0

US-09-966-880a-8 (1-198) x HSM003885 (1-15)
QY      193 PheArgThr 195
DB      14 TTCGGAGCC 6

RESULT 128
ID      HSM007985 standard; mRNA; EST; 15 BP.
XX
XX      AL043135;
XX
XX      AL043135.1
XX

```

```

DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
XX      Homo sapiens mRNA; EST DKFZp434D0823_r1 (from clone DKFZp434D0823)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]
XX      RP 1-15
XX      RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      RT /
XX      RL Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MI MIPs, Am Klopferpitz 18a D-82152 Martinsried, GERMANY
XX
XX      CC Clone from S. Wiemann, sequenced by LMT within the CDNA
XX      CC sequencing consortium of the German Genome Project
XX      CC No s1 sequence available
XX      CC This clone is available at the RZPD in Berlin
XX      CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
XX      FH
XX      FT source      1..15
XX      FT              /db_xref="taxon:9606"
XX      FT              /mol_type="mRNA"
XX      FT              /organism="Homo sapiens"
XX      FT              /clone="DKFZp434D0823"
XX      FT              /clone_1b="434 (synonym: htes3). Vector pSport1; host
XX      FT              DH10B; sites NotI + SalI"
XX      FT              /dev_stage="adult"
XX      FT              /tissue_type="testis"
XX
SQ      Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;
XX
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches:  0
Query Match:    1.52%          Indels:      0
DB:            2            Gaps:        0

US-09-966-880a-8 (1-198) x HSM007985 (1-15)
QY      193 PheArgThr 195
DB      11 TTCGGAGCC 3

RESULT 129
ID      HSM008114 standard; mRNA; EST; 15 BP.
XX
XX      AL043264;
XX
XX      AL043264.1
XX
XX      AL043264.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434L1223_r1 (from clone DKFZp434L1223)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX      [1]

```


RP 1-15
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
 XX
 FH Key Location/Qualifiers
 FT 1.15
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1, host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x HSM008114 (1-15)
 QY 193 PheargThr 195
 DB 11 TTCGGAGCC 3
 RESULT 130
 HSM008148/c standard; mRNA; EST; 15 BP.
 XX
 AC AL0432298;
 XX
 SV AL043298.1
 XX
 DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
 XX
 DE Homo sapiens mRNA; EST DKFZp434M2423_x1 (from clone DKFZp434M2423)
 XX
 KM EST; expressed sequence tag.
 XX
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 XX
 RN 1-15
 RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
 XX
 CC Clone from S. Wiemann, sequenced by LMU within the CDNA
 CC sequencing consortium of the German Genome Project
 CC No s1 sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX
 FH Key Location/Qualifiers
 FT 1.15
 FT /db_xref="taxon:9606"
 FT /mol_type="mRNA"
 FT /organism="Homo sapiens"
 FT /clone_lib="434 (synonym: htes3). Vector pSport1, host
 FT DH10B; sites NotI + SalI"
 FT /dev_stage="adult"
 FT /tissue_type="testis"
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 4 G; 3 T; 0 other;
 Alignment Scores:
 Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 2 Gaps: 0
 US-09-966-880A-8 (1-198) x HSM008148 (1-15)
 QY 193 PheargThr 195
 DB 11 TTCGGAGCC 3
 RESULT 131
 AL931094 15 bp mRNA linear EST 14-NOV-2002
 LOCUS AL931094
 DEFINITION AL931094 NAPI Anopheles gambiae cDNA clone NAPI-P72-D-06-5, mRNA
 sequence.
 ACCESSION AL931094
 VERSION AL931094.1 GI:24973074
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
 Anophelinae;
 1 (bases 1 to 15)
 Christophides G.K., Blass, K., Zdobnov, E.M., Carmouch, R., Benes, V.
 and Kafatos, F.C.
 Anopheles gambiae EST, European Molecular Biology Laboratory
 Unpublished (2002)
 CONTACT: Christophides GK
 FOLIS C. Kafatos laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany
 Tel.: +49 6221 387-440
 Fax: +49 6221 387-306
 Email: christoph@embl-heidelberg.de
 Plate: P72 row: D column: 06.
 FEATURES
 source
 1.15
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="NAPI-P72-D-06-5"
 /lab_host="E. coli DH10B"
 /clone_lib="NAPI"
 /note="Vector: pRT73D-Pac (Pharmacia); Site 1: NotI;
 Site 2: EcoRI; ESTs sequenced from the T7 priming site
 that reads from the 5' end of cDNA. The NAPI is a
 directionally cloned and normalized, oligo-T primed cDNA
 library constructed from a mixture of Anopheles gambiae
 developmental stages according to: Bonaldo, Lennon &
 Soares (1996): Normalization and Subtraction: Two
 Approaches To Facilitate Gene Discovery, Genome Research
 6, 791-806."

ORIGIN

Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AL931094 (1-15)

Qy 172 LeuSerArg 174
 |||||
 2 CTCAGCAGA 10

RESULT 132
 AV199466/c
 LOCUS AV199466 Yui Kohara unpublished cDNA Caenorhabditis elegans cDNA
 DEFINITION AV199466 Yui Kohara unpublished cDNA Caenorhabditis elegans cDNA
 ACCESSION AV199466
 VERSION AV199466.1 GI:5583237
 KEYWORDS EST.
 SOURCE Caenorhabditis elegans
 ORGANISM Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE
 1 (bases 1 to 15)
 Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitani, H., Nishigaki, A., Motomashi, T., Zeng, Q., Matanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.
 Expressed genes in C. elegans
 Unpublished (1999)

TITLE
 JOURNAL
 COMMENT
 Contact: Yui Kohara
 Genome Biology Lab.
 National Institute of Genetics
 Yata 1111, Mishima, Shizuoka 411, Japan
 Tel: 81-559-81-6854
 Fax: 81-559-81-6855
 Email: ykohara@lab.nig.ac.jp.
 Location/Qualifiers

FEATURES
 source
 1. 15
 /organism="Caenorhabditis elegans"
 /mol_type="cDNA"
 /strain="CB1489 hit-8(e1489)"
 /db_xref="taxon:6239"
 /clone="YK5462"
 /sex="hermaphrodite, male"
 /tissue_type="whole animal"
 /dev_stage="varied"
 /clone_lib="Yui Kohara unpublished cDNA"

ORIGIN
 Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AV199466 (1-15)

Qy 25 ArgGluThr 27
 |||||
 11 CGAGAACG 3

RESULT 133
 AM059513
 LOCUS AM059513 15 bp mRNA linear EST 23-AUG-2000
 DEFINITION HUTH_bse.c.dnc15.final.cluster.2 (36) DNC15 Homo sapiens cDNA
 similar to ribosomal protein S17, mRNA sequence.

ACCESSION AM059513
 VERSION AM059513.1 GI:6651835
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 15)
 Brenner, S., Williams, S.R., Vernass, E.H., Storck, T., Moon, K., McColium, C., Mao, J.I., Kirchner, J., Eletri, S., Dubridge, R.B., Burcham, T. and Albrecht, G.
 In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 10677516
 Contact: Burcham TS
 LYNX Therapeutics, Inc.
 25861 Industrial Blvd., Hayward, CA 94545, USA
 Tel: 510 670 9338
 Fax: 510 670 9302
 Email: timbelynxgen.com
 Sequence obtained from LYNX Therapeutics Megasort technology.
 Collected from the down-regulated gate. Consensus sequence of 36 sequences in cluster.
 High quality sequence stop: 15.
 Location/Qualifiers

FEATURES
 source
 1. 15
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_type="monocytic leukemia"
 /cell_line="THP-1 (TIB-202)"
 /clone_lib="DNC15"
 /note="Vector: PCR.1; Cloning of PCR products from micro-beads carrying 3' end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

ORIGIN
 Alignment Scores:

Pred. No.:	3.17e+06	Length:	15
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AM059513 (1-15)

Qy 169 SerValArg 171
 |||||
 4 AGTGTACG 12

RESULT 134
 AM247148
 LOCUS AM247148 15 bp mRNA linear EST 07-JAN-2000
 DEFINITION 2819953.3prime NIH_MGC_7 Homo sapiens cDNA clone IMGB:2819953 3', mRNA sequence.
 ACCESSION AM247148
 VERSION AM247148.1 GI:6590141
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleia; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 15)
 NIH-MGC http://mgc.ncl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Other_ESTs: 2819953.5prime
 Contact: Robert Strauberg, Ph.D.
 Email: cga@ncl.nih.gov
 Tissue Procurement: DCTD/DTP cDNA library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Berkeley WGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnln.gov/bbrp/image/image.html Base Calling / Quality Trimming: cross_match from University of Washington Genome Center. Vector PHRAP suite. Poly-T identification: patmatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 13 contiguous PHRD high quality bases following vector sequence. Very low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: L10W2 row: P column: 2
High quality sequence stop: 13.
Location/Qualifiers

FEATURES
source
1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2819953"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NH MGC 7"
/note="Organ: lung; Vector: pOT7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 10 Gaps: 0

US-09-966-880A-8 (1-198) X AM247148 (1-15)
CY 61 PhelanArg 63
Db 6 TTTTACGG 14
RESULT 135
BG900900/c 15 bp mRNA linear EST 06-NOV-2001
LOCUS HOA7-1-A8 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.
ACCESSION BG900900 GI:14311149
VERSION BG900900.1 GI:14311149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathé,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651

FEATURES
source
1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT 1; Site 1: SalI; Site 2: NotI; Directional"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) X BG900900 (1-15)
CY 132 AlagiyVal 134
Db 9 GCGACGCTA 1
RESULT 136
BG925415
LOCUS HNC5-1-B1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION HNC5-1-B1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA sequence.
ACCESSION BG925415
VERSION BG925415.1 GI:14319938
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathé,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.
TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE 21482651
COMMENT
PUBMED 11597177
CONTACT: Sanjay Kumar
UN2109
GlasgowKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.
Location/Qualifiers
1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E. coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"

ORIGIN /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

ALIGNMENT SCORES:

Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925415 (1-15)

QY 104 Leuserleu 106

DB 2 CTCCTCTCT 10

RESULT 137

BG925415/c

LOCUS BG925415 15 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC5-1-B1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA

ACCESSION BG925415

VERSION BG925415.1 GI:1431938

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 15)

AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,

Sathe,G., Wei,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M., and

Lark,M.W.

IDENTIFICATION AND INITIAL CHARACTERIZATION OF 5000 EXPRESSED

SEQUENCED TAGS (ESTs) EACH FROM ADULT HUMAN NORMAL AND

OSTEOARTHRITIC CARTILAGE CDNA LIBRARIES

JOURNAL Osteoarthritis Cartilage 9 (7), 641-653 (2001)

MEDLINE 11597177

PUBMED 11597177

COMMENT Contact: Sanjay Kumar

UN2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@sk.com

Seq primer: T7.

Location/Qualifiers

1. 15

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cissue_type="cartilage"

/lab_host="E.coli DH10 B"

/clone_id="HNC (Human Normal Cartilage)"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925415 (1-15)

QY 24 ArgArgGlu 26

DB 12 AGAAGAGAG 4

RESULT 138

BM396203

LOCUS BM396203

DEFINITION 5009-0-18-G08.c.1 Chiloat/Turkewitz cDNA (large fraction)

ACCESSION BM396203

VERSION BM396203.1 GI:18196256

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 15)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,

Frankel,U., and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

CONTACT: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. 15

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_id="Chiloat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK-; Details on library

preparation can be found in Chiloat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

QY 83 SerTTPSer 85

DB 6 AGCTGGAGC 14

RESULT 139

BM396203/c

LOCUS BM396203

DEFINITION 5009-0-18-G08.c.1 Chiloat/Turkewitz cDNA (large fraction)

ACCESSION BM396203

VERSION BM396203.1 GI:18196256

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 15)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orías,E., Kirk,K.E.,

Frankel,U., and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.

FEATURES

Location/Qualifiers
 1..15
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM396203 (1-15)

Qy 41 SerPheSer 43

Db 9 AGCTTTTCA 1

RESULT 140

BM398486

LOCUS

DEFINITION 15 bp mRNA linear EST 17-JAN-2002

tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM398486 GI:18198539

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1..15

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM398486 (1-15)

Qy 111 AlaaArgLeu 113

Db 7 GCTCGGCTT 15

RESULT 141

BM415446

LOCUS

DEFINITION 15 bp mRNA linear EST 28-JAN-2002

Op20520 Mixed Stage EST's from Globodera pallida, the potato cyst nematode Globodera pallida cDNA, mRNA sequence.

ACCESSION

BM415446

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: Opperman, C

Center for the Biology of Nematode Parasitism

NC State University; IACR-Rothamsted

Campus Box 7616; Raleigh, NC 27695, USA

Tel: 919.515.6699

Fax: 919.515.9500

Email: warthog@ncsu.edu

Gt11-4PCN.F.D05.PCN.4.F.042.ab1.

Location/Qualifiers

1..15

/organism="Globodera pallida"

/mol_type="mRNA"

/db_xref="taxon:36090"

/clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode"

/note="Vector: lambda GT11; This is a collaborative effort between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM415446 (1-15)

Qy 42 PheSerLeu 44

Db 2 TTCACTCTA 10

RESULT 142

BO584986

LOCUS

DEFINITION 15 bp mRNA linear EST 06-DEC-2002

BO11826-024-002-K24-SP6 MP12-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-002-K24 5-PRIME, mRNA sequence.

ACCESSION

BO584986

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plate: 2 row: K column: 24
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1..15
 /organism="Beta vulgaris"
 /mol_type="cDNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:181716"
 /db_xref="taxon:161934"
 /clone="024-002-K24"
 /tissue_type="inflorescence"
 /lab_host="EMDH10B"
 /clone_1lb="MP1Z-ADIS-024-inflorescence"
 /note="Vector: PCWMSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleimanzelebener Saatnucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-BEET
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ584986 (1-15)

QY 179 Tlepeulen 181
 |||||
 9 ATTCTCTCA 1

RESULT 143
 BQ588286 15 bp mRNA linear EST 06-DEC-2002
 LOCUS B012308-024-008-J22-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
 DEFINITION 024-008-J22 5-PRIME, mRNA sequence.
 ACCESSION BQ588286
 VERSION BQ588286.1 GI:26117869
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 15)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.

REFERENCE
 AUTHORS

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189
 PUBMED 12472698
 COMMENT Contact: Weishaar B
 ADIS DNA core facility at MPIZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mpiz-koeln.mpg.de
 Insert Length: 15 Std Error: 0.00
 Plate: 8 row: J column: 22
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.
 Location/Qualifiers
 1..15
 /organism="Beta vulgaris"
 /mol_type="cDNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding
 line)"
 /db_xref="GABI:184558"
 /db_xref="taxon:161934"
 /clone="024-008-J22"
 /tissue_type="leaf"
 /lab_host="EMDH10B"
 /clone_1lb="MP1Z-ADIS-024-leaf"
 /note="Vector: PCWMSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleimanzelebener Saatnucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-BEET
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ588286 (1-15)

QY 36 Argäpser 38
 |||||
 1 CGTCTTCC 9

RESULT 144
 BQ589356 15 bp mRNA linear EST 06-DEC-2002
 LOCUS B014008-024-015-K22-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
 DEFINITION cDNA clone 024-015-K22 5-PRIME, mRNA sequence.
 ACCESSION BQ589356
 VERSION BQ589356.1 GI:26118939
 KEYWORDS EST.
 SOURCE Beta vulgaris
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 15)
 Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 JOURNAL Plant J. 32 (5), 845-857 (2002)
 MEDLINE 22362189

REFERENCE
 AUTHORS

PUBMED
COMMENT

12472698
Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 15 row: K column: 22
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. 15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:187717"
/db_xref="taxon:161934"
/clone="024-015-K22"
/tissue_type="storage root"
/lab_host="EMD10B"
/clone_lib="MPiZ-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ589356 (1-15)

CY 172 leuserArg 174
|||||

DB 2 TTATCAAGA 10

RESULT 145 15 bp mRNA linear EST 06-DEC-2002
BQ591870/c
LOCUS E012551-024-016-M20-SP6 MPiZ-ADIS-024-storage root Beta vulgaris

DEFINITION cDNA clone 024-016-M20 5-PRIME, mRNA sequence.
BQ591870
BQ591870.1 GI:26121453

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant U. 32 (5), 845-857 (2002)

Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research

FEATURES
source

Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Plate: 16 row: M column: 20
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
1. 15
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/tissue_type="storage root"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzeleberer Saatnucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-SalI-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591870 (1-15)

CY 131 ArgAlaGly 133
|||||

DB 9 CGCGCTGGG 1

RESULT 146

BQ595631/c 15 bp mRNA linear EST 06-DEC-2002
LOCUS E012693-024-022-B04-SP6 MPiZ-ADIS-024-developing root Beta vulgaris

DEFINITION cDNA clone 024-022-B04 5-PRIME, mRNA sequence.
BQ595631
BQ595631.1 GI:26125214

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE
AUTHORS
1 (bases 1 to 15)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
Plant U. 32 (5), 845-857 (2002)

Contact: Weishaar B
ADIS DNA core facility at MPiZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00

Plate: 22 row: B column: 04
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES
source

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/issue_type="developing root"
/lab_host="BMDH10B"
/clone_lib="MP12-ADIS-024-developing root"
/note="Vector: PCWVSORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleimanzeleber Saatzzucht AG Einbeck, Germany, contact: b.schulz@kms.de; cloning site SalI-NotI, primer sites and orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Best project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ595631 (1-15)

QY 22 LysGlyArg 24
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13 AAGGACGA 5

Db 13 AAGGACGA 5

RESULT 147

CA796369 15 bp mRNA linear EST 05-DEC-2002
LOCUS CAC.BL.3383 CAC.BL. (Bean and leaf from Amelionardo type Cacao)

DEFINITION Theobroma cacao cDNA clone CAC.BL.3383 5', mRNA sequence.

ACCESSION CA796369.1 GI:26053445

VERSION EST.

KEYWORDS Theobroma cacao (cacao)

SOURCE Theobroma cacao

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae; Theobroma.

REFERENCE 1 (bases 1 to 15)

AUTHORS Jones, P.G., Allaway, D., Gilmour, D.M., Harris, C., Rankin, D., Retzel, E.R. and Jones, C.A.

TITLE Gene discovery and microarray analysis of cacao (Theobroma cacao L.) varieties

JOURNAL Planta 216 (2), 255-264 (2002)

MEDLINE 22337596

PUBMED 12447539

COMMENT Contact: Jones, Paul

Masterfoods

3d Dundee Road, Slough, Berkshire, UK, SL1 4UG

Tel: +44 1664 416644

Email: Paul.jones@eu.affem.com

Seq primer: T3;

Location/Qualifiers

FEATURES
source

1. .15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelionardo type"

ORIGIN

Alignment Scores:

Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CA796369 (1-15)

QY 157 ArgThrPhe 159
|||
5 AGGACCTT 13

Db 5 AGGACCTT 13

RESULT 148

CF303956 15 bp mRNA linear EST 15-AUG-2003
LOCUS ABF1--03-K24 g1 ABF3-overexpressing transgenic rice lambda phage

DEFINITION cDNA library (ABF1) Oryza sativa cDNA clone ABF1--03-K24, mRNA sequence.

ACCESSION CF303956

VERSION CF303956.1 GI:33675717

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

FEATURES
source

1. .15
/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF1--03-K24"

/issue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E. coli SOLR"

/clone_lib="ABF3-overexpressing transgenic rice lambda phage cDNA library (ABF1)"

/note="Vector: plasmid SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

ORIGIN

Alignment Scores:

1. .15
/organism="Theobroma cacao"
/mol_type="mRNA"
/strain="Amelionardo type"

Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x CF315668 (1-15)
 QY 124 Glu1yleu 126
 DB 5 GAGGATTA 13
 RESULT 149
 CF315668 15 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--04-K19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 DEFINITION
 ACCESSION CF315668
 VERSION CF315668.1 GI:33687429
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 15)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..15
 /organism="Oryza sativa"
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 /db_xref="taxon:4530"
 /clone="HD--04-K19"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

LOCUS CF316846 15 bp mRNA linear EST 15-AUG-2003
 DEFINITION HD--06-F02.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--06-F02, mRNA sequence.
 ACCESSION CF316846
 VERSION CF316846.1 GI:33688607
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 15)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)
 Contact: Nahm B.H.
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
 Location/Qualifiers
 1..15
 /organism="Oryza sativa"
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 /db_xref="taxon:4530"
 /clone="HD--06-F02"
 /tissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 2 weeks"
 /lab_host="E.coli DH10B"
 /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
 cDNA library (HD)"
 /note="Vector: pCR4-TOPO, Site 1: EcoRI; Callus was
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was
 reverse transcribed and then used for PCR. mRNA was
 derived from rice Histone Deacetylase overexpression
 line."

ORIGIN
 Alignment Scores:
 Pred. No.: 3.17e+06 Length: 15
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x CF316846 (1-15)
 QY 49 LeuArgaen 51
 DB 3 CTACTAAC 11
 RESULT 151
 CF317855 15 bp mRNA linear EST 15-AUG-2003
 LOCUS HD--07-L05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
 library (HD) Oryza sativa cDNA clone HD--07-L05, mRNA sequence.
 ACCESSION CF317855
 VERSION CF317855.1 GI:33689616
 KEYWORDS EST.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 15)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL
COMMENT

Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDA1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.17e+06	3.00	15	3	0	0	0	0
Percent Similarity:	100.00%						
Best Local Similarity:	100.00%						
Query Match:	1.52%						

US-09-966-880A-8 (1-198) x CF317855 (1-15)

Qy 59 leu|eup|e 61

Db 14 TTATTATTC 6

RESULT 152

LOCUS CF324208 15 bp mRNA linear EST 18-AUG-2003

DEFINITION HDN--05-018.g1 OSHDA1-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa CDNA clone HDN--05-018, mRNA
sequence.

ACCESSION CF324208

VERSION CF324208.1 GI:33796681

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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1..15
/organism="Oryza sativa"
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/cultivar="Nackdong"
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ORIGIN

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/clone="HDN--05-018"
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/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage CDNA library II (HDN)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.17e+06	3.00	15	3	0	0	0	0
Percent Similarity:	100.00%						
Best Local Similarity:	100.00%						
Query Match:	1.52%						

US-09-966-880A-8 (1-198) x CF324208 (1-15)

Qy 142 Lys|Asp|Tyr 144

Db 5 AAGGATTAC 13

RESULT 153

LOCUS CF324208/C 15 bp mRNA linear EST 18-AUG-2003

DEFINITION HDN--05-018.g1 OSHDA1-overexpressing transgenic rice lambda phage
CDNA library II (HDN) Oryza sativa CDNA clone HDN--05-018, mRNA
sequence.

ACCESSION CF324208

VERSION CF324208.1 GI:33796681

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

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1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDN--05-018"
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/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDA1-overexpressing transgenic rice lambda
phage CDNA library II (HDN)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

ORIGIN

Alignment Scores:

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Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF340248 (1-15)

QY 100 Glyaspro 102
DB 14 GATATCCT 6

RESULT 154
LOCUS CF340244/c 15 bp mRNA linear EST 18-AUG-2003
DEFINITION RCL1--07-G18_g1 Regenerated callus lambda phage cDNA library (RCL1)
ORIGIN Oryza sativa cDNA clone RCL1--07-G18, mRNA sequence.
ACCESSION CF340244
VERSION CF340244.1 GI:33828846
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.U., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahn,B.H.
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahn B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnaah@gbio.com, bhnaah@bio.myongji.ac.kr.
location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="RCL1--07-G18"
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/lab_host="E.coli SOLR"
/clone_lib="Regenerated callus lambda phage cDNA library (RCL1)"
/note="Vector: pBluescript SK(+), Site 1: SstI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 3hrs on regenerated media"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF340244 (1-15)

QY 165 leuhiaslu 167
DB 15 CTTCATGAG 7

RESULT 155
LOCUS CF543306/c
DEFINITION
ACCESSION

```

```

LOCUS CF543306 15 bp mRNA linear EST 22-SEP-2003
DEFINITION S014668-024-029-F24-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION CF543306
VERSION CF543306.1 GI:34691746
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Magnoliophyta; Magnoliopsida; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 15)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehnach,H.
and Radefeld,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL MEDLINE
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mplz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
Place: 29 row: F column: 24
Seq primer: SP6.
location/Qualifiers
1..15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:936441"
/db_xref="taxon:161934"
/clone="024-029-F24"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP12-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzelebener Saatnucht AG Binbeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BEET project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.17e+06 Length: 15
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF543306 (1-15)

QY 193 Pheargthr 195
DB 15 TTTCGACG 7

RESULT 156
LOCUS CF543404/c 15 bp mRNA linear EST 22-SEP-2003
DEFINITION S014668-024-029-D20-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION CF543404

```

```

VERSION      CF543404.1  GI:34891844
KEYWORDS
SOURCE       Beta vulgaris
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Caryophyllales; Magnoliophyta; eudicotyledons; core eudicots;
              Spermatophytes; Amaranthaceae; Beta.
REFERENCE    1 (bases 1 to 15)
              Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
              Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
              Plant J. 32 (5), 845-857 (2002)
JOURNAL      22362189
MEDLINE
PUBMED
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MPZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mpz-koeln.mpg.de
              Insert Length: 15 Std Error: 0.00
              Plate: 29 Row: D Column: 20
              Seq primer: SP6.

FEATURES
source       1..15
              Location/Qualifiers
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultiyar="KMS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:936359"
              /db_xref="taxon:161934"
              /clone="024-029-D20"
              /tissue_type="leaf"
              /lab_host="EMDHI08"
              /clone_idb="MP12-ADIS-024-leaf"
              /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet, library provided by KMS
              Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-SalI-CCAGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-BEET
              Project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%         Indels:        0
DB:             14           Gaps:         0

US-09-966-880a-8 (1-198) x CF543404 (1-15)

QY      193 PheargThr 195
        |||||
        15 TTTCGACG 7

RESULT 157
R41075      15 bp      mRNA      linear      EST 16-MAY-1995
LOCUS      Hk082-f Adult heart, Clontech Homo sapiens cDNA clone K082-f, mRNA
DEFINITION Sequence.
ACCESSION  R41075
VERSION    R41075.1 GI:798691
KEYWORDS  EST.
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE    1 (bases 1 to 15)
              Wray,M.M.Y., Cheung,H.K.Y., Lam,M.Y., Law,P.T.W., Lo,A.S.Y.,
              Lui,V.W.Y., Luk,S.C.W., Tsui,S.K.W., Tung,C.K.C., Yam,N.Y.H.,
              Liaw,C.C. and Lee,C.Y.
              Gene expression of adult human heart as revealed by random
              sequencing of cDNA library
              Miami Winter Biotechnol. Symp. Proc. 6, 90 (1995)
JOURNAL      22362189
MEDLINE
PUBMED
COMMENT      Department of Biochemistry
              The Chinese University of Hong Kong
              Rm 302C, Basic Medical Science Building, The Chinese University of
              Hong Kong, Shatin, N.T., Hong Kong.
              Tel: 8526096874
              Fax: 8526035123
              Email: bl33723@vax.csc.cuhk.hk
              Seq primer: GGTGGCGACGCTCTGGAGCC.

FEATURES
source       1..15
              Location/Qualifiers
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="K082-f"
              /lab_host="E. coli Y1090"
              /clone_idb="Adult heart, Clontech"
              /note="Vector: Lambda gII1, Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Alignment Scores:
Pred. No.:      3.17e+06      Length:      15
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%         Indels:        0
DB:             14           Gaps:         0

US-09-966-880a-8 (1-198) x R41075 (1-15)

QY      170 VALArgLeu 172
        |||||
        3 GTGCGATTG 11

RESULT 158
HSK001764
ID      HSK001764      standard; mRNA; EST; 16 BP.
AC      AL037434;
XX
XX      AL037434.1
XX
XX      AL037434.1
XX
SV      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE      Homo sapiens mRNA; EST DKFZps56401471_s1 (from clone DKFZps56401471)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC      Submitted (12-MAR-1999) to the EMBL/Genbank/DBJ databases.
RL      M1P8, Km Kioferepitz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by GBF within the cDNA
XX      sequencing consortium of the German Genome Project
XX      No r1 sequence available
XX      This clone is available at the RZPD in Berlin

```

```

CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp56401471"
FT /clone_lib="564 (synonym: hfbz2) . Vector pAMP1; host
FT X1-2blue, sites NotI + SalI"
FT /dev_stage="fetal"
FT /tissue_type="brain"
XX
SQ Sequence 16 BP; 5 A; 1 C; 0 G; 10 T; 0 other;

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSM001764 (1-16)

Cy 60 Leupheleu 62
Db 3 TTATTTTTA 11

RESULT 159
HSM004270/c standard; mRNA; EST; 16 BP.
ID HSM004270
XX
AC AL039794.1
XX
SV AL039794.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434B1612_x1 (from clone DKFZp434B1612)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
RN [1]
RP 1-16
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIR3, Am Klopfererwitz 18a D-82152 Martinsried, GERMANY
XX
XX Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No. 81 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..16
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp434B1612"
FT /clone_lib="434 (synonym: htest) . Vector pSport1; host
FT DH10B; sites NotI + SalI"

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FT /dev_stage="adult"
FT /tissue_type="testis"
XX
SQ Sequence 16 BP; 3 A; 4 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 2 Gaps: 0

US-09-966-880A-8 (1-198) x HSM004270 (1-16)

Cy 193 PheargTnr 195
Db 14 TTCCGAGAC 6

RESULT 160
AA904711/c 16 bp mRNA linear EST 09-JUN-1998
OJ74d10.81 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1504051 3' similar to TR:015387 015387 34 KDA MOV34 ISOLOGUE.
DEFINITION
AA904711
AA904711.1 GI:3039834
ACCESSION
AA904711
VERSION
AA904711.1 GI:3039834
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 16)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.lln.gov) for further information.
Trace considered overall poor quality
Insert length: 1732 Std Error: 0.00
Seg primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cdb_xref="IMAGE:1504051"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCT CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0

```

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA939272 (1-16)

QY 154 AsnHISGLU 156

DB 10 AATCATGAG 2

RESULT 161
AA939272/cLOCUS 16 bp mRNA linear EST 01-MAY-1998
DEFINITION Oq31b06.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587923 3'similar to SW:CA34 HUMAN Q01955 PROCOLLAGEN ALPHA 3 (IV) CHAIN
PRECUSOR, contains OFR.b3 MSRI repetitive element ;, mRNA
sequence.

ACCESSION AA939272 GI:3099185

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.REFERENCE 1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
cDNA distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:

www.bio.lml.gov/bbtp/image/image.html

Trace considered overall poor quality

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.
Location/Qualifiers1. .16
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1587923"

/tissue_type="pooled germ cell tumors"

/lab_host="DH10B"

/clone_lib="NCI CGAP GC4"

/note="Vector: pRT3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pRT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA939272 (1-16)

QY 100 GIYAAspPro 102

DB 15 GGAAACCCC 7

RESULT 162

AA953804/c

LOCUS 16 bp mRNA linear EST 07-JUL-1998

DEFINITION O038c06.s1 NCI CGAP Lm5 Homo sapiens cDNA clone IMAGE:1568458 3'
similar to TR:000278 000278 LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH
7. [2] TR:000280 ;, mRNA sequence.

ACCESSION AA953804 GI:3116722

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.REFERENCE 1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
cDNA distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LML at:

www.bio.lml.gov/bbtp/image/image.html

Trace considered overall poor quality

Insert length: 434 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.
Location/Qualifiers1. .16
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1568458"

/tissue_type="carcinoid"

/lab_host="DH10B"

/clone_lib="NCI CGAP Lm5"

/note="Organ: lung; Vector: pRT3D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
neuroendocrine lung carcinoid, and was then primed with a
Not I - oligo(dT) primer. Double-stranded cDNA was ligated
to Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pRT73 vector. Library is normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA953804 (1-16)

QY 171 ArgLeuSer 173

DB 9 CGCTTGAGC 1

RESULT 163

AA968729

LOCUS 16 bp mRNA linear EST 27-AUG-1998

DEFINITION O09h11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:160157 3'
similar to SW:FRPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION AA968729
 VERSION AA968729.1 GI:3143909
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: www.bio.lnu.gov/bbrp/image/image.html

FEATURES
 source
 1.16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1601157"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_1ib="NCI CGAP GC3"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Alignment Scores:
 Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x AA968729 (1-16)

QY 23 GYATGATG 25
 |||||
 5 GCGAGGAGG 13

RESULT 164
 AA968729/c 16 bp mRNA linear EST 27-AUG-1998
 LOCUS aa968729.1
 DEFINITION similar to SW:PBPE HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E ; contains element MSRI repetitive element ;, mRNA sequence.
 ACCESSION AA968729
 VERSION AA968729.1 GI:3143909
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: www.bio.lnu.gov/bbrp/image/image.html

FEATURES
 source
 1.16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1601157"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /clone_1ib="NCI CGAP GC3"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
 Alignment Scores:
 Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x AA968729 (1-16)

QY 180 LeuLeuPro 182
 |||||
 12 CTCCTCCCC 4

RESULT 165
 A1094839/c 16 bp mRNA linear EST 18-AUG-1998
 LOCUS ga22c08.x1
 DEFINITION similar to TR:O00599 O00599 CON1. ; contains element MSRI repetitive element ;, mRNA sequence.
 ACCESSION A1094839
 VERSION A1094839.1 GI:3433815
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 16)
 AUTHORS NCI/NINDS-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/RTGAP), Tumor Gene Index
 JOURNAL Unpublished (1998)
 COMMENT Contact: Robert Strausberg, Ph.D.


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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1838200"
/sex="male"
/lab_host="MDH10B"
/clone_lib="Soares testis_NHT"
/note="Vector: pT7D-Pac (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
primer [5',
TGTTCACCAATCTGAAGTGGAGCGCGCCCAATTTTCTTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

```

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.39e+06	3.00	100.00%	100.00%	1.52%	9	16	3	0	0	0	0

US-09-966-880A-8 (1-198) x A1208066 (1-16)

Oy 77 ArgValThr 79

Db 2 CGGTCACG 10

RESULT 168
LOCUS A1603831

DEFINITION SMOV3MCM27A07SK Onchocerca volvulus molting L3 larva cDNA
(SI96MTM-Ovml3) Onchocerca volvulus cDNA clone SMOV3MCM27A07 5',
mRNA sequence.

ACCESSION A1603831

VERSION A1603831.1 GI:4612980

KEYWORDS EST.

SOURCE

ORGANISM

Onchocerca volvulus
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Onchocerca.
1 (bases 1 to 16)
Williams, S.A., Lizotte-Waniewski, M., Laney, S. and Lustigman, S.
Genes expressed in molting L3 larvae of Onchocerca volvulus
Unpublished (1997)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: Bluescript SK.

FEATURES

source

```

1..16
Location/Qualifiers
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Xumba, Cameroons"
/db_xref="taxon:6282"
/clone="SMOV3MCM27A07"
/dev_stage="molting L3"
/lab_host="XLI-Blue MRP"
/clone_lib="Onchocerca volvulus molting L3 larva cDNA
(SI96MTM-Ovml3)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Filarial nematode parasite of humans. Third-stage

```

larvae, L3, were isolated from infected black flies in Cameroon (forest strain). The L3 were cultured in 20% FCS in IMDM+ NCTC 135 and collected after day 1, 2, or 3 in culture. L3 of O. volvulus molt to fourth-stage larvae by day 5 in culture. mRNA was isolated from approximately 6000 molting larvae (ml3), 2000 larvae from day 1, 2 or 3 in culture, and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library was constructed in the lambda Uni-Zap XR vector and has 1 x 10⁶ independent recombinants and the average insert size is ~1200 bp. The library was constructed by Sara Lustigman and Michelle Lizotte-Waniewski in the Laboratory of Dr. S. A. Williams. The library is available from Dr. Sara Lustigman (email: slustigman@bc.org)."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.39e+06	3.00	100.00%	100.00%	1.52%	9	16	3	0	0	0	0

US-09-966-880A-8 (1-198) x A1603831 (1-16)

Oy 48 TyrLeuArg 50

Db 3 TATTTAAG 11

RESULT 169
LOCUS AM248540

DEFINITION 2820844.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820844 3',
mRNA sequence.

ACCESSION AM248540

VERSION AM248540.1 GI:6591533

KEYWORDS EST.

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 16)
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Other ESTs: 2820844.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (ILMI) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/ILMI at:
www.bio.lnml.gov/bdrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 15
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: trace file contained 16 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LHCMS row: E column: 5
High quality sequence stop: 15.

FEATURES

source

```

1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"

```

/db_xref="taxon:9606"
 /clone="IMAGE:2820844"
 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM250981 (1-16)

CY 15 Pheylsaa 17

DB 8 TTTAAAC 16

RESULT 170

AM250981/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AM250981 16 bp mRNA linear EST 07-JAN-2000
 2822267.3prime NIH_MGC_7 Homo sapiens CDNA clone IMAGE:2822267 3',
 mRNA sequence.
 AM250981
 AM250981.1 GI:6594070
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 16)
 NIH-MGC http://mgi.nci.nih.gov/
 Unpublished (1999)
 Other ESTs: 2822267.5prime
 Contact: Robert Strauberg, Ph.D.
 Email: cgsbds-remail.nih.gov
 Tissue Procurement: DCTD/DTF CDNA Library Preparation: Ling
 Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LIML) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LIML at:
 www.bio.liml.gov/bbtp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center. Vector
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
 Drosophila Genome Project. University of Washington Genome Center:
 http://www.genome.washington.edu/Low Quality Sequence: 9 contiguous
 PHRED high quality bases following vector sequence. Very Low
 Quality Sequence: trace file contained 16 contiguous distinct peaks
 following vector sequence. Polyadenylation: Based upon the presence
 of a XhoI site followed by a run of 14 or more T residues at the
 beginning of the sequence, this CDNA insert was polyadenylated.
 Plate: L16M8 row: 8 column: 12
 High quality sequence stop: 9.
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2822267"

FEATURES

source

/tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AM250981 (1-16)

CY 118 Asparglys 120

DB 16 GACAGGAAA 8

RESULT 171

BG897738

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BG897738 16 bp mRNA linear EST 06-NOV-2001
 BG897738
 HOA17-1-C3 HOA (Human Osteoarthritic Cartilage) Homo sapiens CDNA,
 mRNA sequence.
 BG897738
 BG897738.1 GI:14307987
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 16)
 Kumar, S., Connor, J.R., Dadds, R.A., Halsey, W., Van Horn, M., Mao, J.,
 Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
 Larr, M.W.
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage CDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21462651
 MEDLINE
 11597177
 PUBMED
 Contact: Sanjay Kumar
 UW2109
 GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@gsk.com
 Seq primer: 77,
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="HOA (Human Osteoarthritic Cartilage)"
 /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
 Directional"

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 1.52%
 DB: 12
 Gaps: 0

US-09-966-880A-8 (1-198) x BG977738 (1-16)

QY 174 ArginLeu 176
 DB 8 AGGAGCTC 16

RESULT 172
 BG900981

LOCUS H0A52-1-D1.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
 DEFINITION
 ACCESSION BG900981
 VERSION BG900981.1 GI:14311230
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
 Lark,M.W.
 1 (bases 1 to 16)
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651
 11597177
 Contact: Sanjay Kumar
 UW2109

REFERENCE
 AUTHORS

TITLE

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@gsk.com
 Seq primer: T7.
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_id="HOA (Human Osteoarthritic Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

ORIGIN

Alignment Scores:
 Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG900981 (1-16)

QY 41 SerPheSer 43
 DB 3 AGCTTAGC 11

RESULT 173
 BG926060
 LOCUS HNC23-1-E1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
 DEFINITION
 ACCESSION BG926060

VERSION BG926060.1 GI:14320583
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
 Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
 Lark,M.W.
 1 (bases 1 to 16)
 Identification and initial characterization of 5000 expressed
 sequenced tags (ESTs) each from adult human normal and
 osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 21482651
 11597177
 Contact: Sanjay Kumar
 UW2109

REFERENCE
 AUTHORS

TITLE

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

FEATURES
 source

GlaxoSmithKline
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@gsk.com
 Seq primer: T7.
 Location/Qualifiers
 1..16
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="cartilage"
 /lab_host="E.coli DH10 B"
 /clone_id="HNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
 Directional"

ORIGIN

Alignment Scores:
 Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG926060 (1-16)

QY 34 LysArgArg 36
 DB 9 AAGAGAGG 1

RESULT 174
 BM397104/c

LOCUS BM397104 16 bp mRNA linear EST 17-JAN-2002
 DEFINITION 5009-0-28-H09.c.2 Chilcoac/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 BM397104
 ACCESSION BM397104.1 GI:18197157
 VERSION
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 ORGANISM Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Tetrahymenozoa; Tetrahymenina; Tetrahymena.
 Turkewitz,A.P., Karrer,K.M., Jahn,C., Ortae,E., Kirk,K.E.,
 Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172

REFERENCE

AUTHORS
 TITLE
 JOURNAL
 COMMENT

Email: apurkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

source
Location/Qualifiers
1..16
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chlicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM397104 (1-16)

OY 77 ArgValThr 79

DB 14 CGCGTGAAG 6

RESULT 175

BM399406 16 bp mRNA linear EST 17-JAN-2002

LOCUS 5009-0-57-D08.t.2 Chlicoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM399406

VERSION BM399406.1 GI:18199459

KEYWORDS EST.

SOURCE

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 16)

Turkewitz, A.P., Karer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apurkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1..16

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chlicoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM399406 (1-16)

OY 125 GlyLeuArg 127

DB 8 GGATTAAAG 16

RESULT 176

BM401358 16 bp mRNA linear EST 17-JAN-2002

LOCUS 5009-0-9-D08.t.1 Chlicoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM401358

VERSION BM401358.1 GI:18201411

KEYWORDS EST.

SOURCE

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 16)

Turkewitz, A.P., Karer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apurkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1..16

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chlicoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chlicoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM401358 (1-16)

OY 77 ArgValThr 79

DB 13 CGCGTGAAG 5

RESULT 177

BM817126 16 bp mRNA linear EST 05-MAR-2002

LOCUS HC02D04.T3.ab1 HC Hordeum vulgare subsp. vulgare cDNA clone

DEFINITION HC02D04.T3.ab1, mRNA sequence.

ACCESSION BM817126

VERSION BM817126.1 GI:19153140

KEYWORDS EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 16)

Ozturk, N.Z., Michalowski, C.B., Brazille, S., Borchert, C.,

Palacio, C., Normand, C., Murphy, C., Kelley, R., Sant, S.A.,

TITLE
McLaughlin, H., Fredrickson, M.A. and Bohner, H.J.
Monitoring large-scale changes in transcript abundance in drought-
and salt-stressed barley
JOURNAL
Unpublished (2002)
COMMENT
Contact: Mark A. Fredrickson
Plant Biology
University of Illinois
1201 W Gregory Dr, Urbana, IL 61801, USA
Tel: 2172655473
Email: bohnert@life.uiuc.edu.

FEATURES
source
1..16
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mrna"
/strain="cv tokax"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HC02D04.T3.ab1"
/issue_type="Roc"
/dev_stage="3 week old"
/clone_lib="HC"
/note="6 and 10 hour drought stress by placing plants on
moist paper (75% rel. humidity) in light"

ORIGIN
Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BW817126 (1-16)

QY 133 GLYVALGN 135
DB 11 GGGGTACAA 3

RESULT 178
BQ585399 16 bp mRNA linear EST 06-DEC-2002
LOCUS S011421-024-001-L05-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris
DEFINITION CDNA clone 024-001-L05-5-PRIME, mRNA sequence.
ACCESSION BQ585399
VERSION BQ585399.1 GI:26114981
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herrig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnach, H.
and Radclouf, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 1 row: 1 column: 05
Seq primer: SP6; ATTAGTGACACTATAGAGA.
Location/Qualifiers
1..16
/organism="Beta vulgaris"

FEATURES
source
1..16
/organism="Beta vulgaris"

/mol_type="mrna"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:181306"
/db_xref="taxon:161934"
/clone="024-001-L05"
/issue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/note="Vector: PCWVS-PORT6, Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinanleberer Saatnucht AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

ORIGIN
Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ585399 (1-16)

QY 132 ALAGLYVAL 134
DB 3 GCTGCTGTA 11

RESULT 179
BQ586020 16 bp mRNA linear EST 06-DEC-2002
LOCUS B012394-024-013-N21-SP6 MP1Z-ADIS-024-leaf Beta vulgaris CDNA clone
DEFINITION 024-013-N21-5-PRIME, mRNA sequence.
ACCESSION BQ586020
VERSION BQ586020.1 GI:26115602
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 16)
Herrig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfach, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehnach, H.
and Radclouf, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 13 row: N column: 21
Seq primer: SP6; CATACGATTGCTGACACTATAG.
Location/Qualifiers
1..16
/organism="Beta vulgaris"
/mol_type="mrna"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186842"

FEATURES
source
1..16
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/mol_type="mrna"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:186842"

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/db_xref="taxon:161934"
/clone="024-013-N21"
/issue_type="leaf"
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/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586219 (1-16)

QY 11 PhleuTYR 13
Db 2 TTTCTATT 10

RESULT 180
BQ586219 16 bp mRNA linear EST 06-DEC-2002
LOCUS E012392-024-013-Cl9-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION BQ586219
ACCESSION BQ586219
VERSION BQ586219.1 GI:26115801
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Beta vulgaris
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant U. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 13 row: C column: 19
Seg primer: SP6; CATACGATTAGCGACACATATAG.
Location/Qualifiers
1. 16
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/cultivar="KMS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:186651"
/db_xref="taxon:161934"
/clone="024-013-Cl9"
/issue_type="leaf"
/lab_host="EMDH10B"

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/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN

Alignment Scores:
Pred. No.: 3.39e+06 Length: 16
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ586219 (1-16)

QY 109 PhetHrAla 111
Db 10 TTTACGCA 2

RESULT 181
BQ587767 16 bp mRNA linear EST 06-DEC-2002
LOCUS E012340W-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
DEFINITION BQ587767
ACCESSION BQ587767
VERSION BQ587767.1 GI:26117349
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE Beta vulgaris
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant U. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 10 row: M column: 01
Seg primer: SP6; CATACGATTAGCGACACATATAG.
Location/Qualifiers
1. 16
/organism="Beta vulgaris"
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/cultivar="KMS2320 (double haploid, monogerm breeding line)"
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/clone="024-010-M01"
/issue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:

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b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation.
 SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.39e+06	3.00	100.00%	100.00%	1.52%	16	3	0	0	0	0

DB:

13

US-09-966-880A-8 (1-198) x BQ587767 (1-16)

QY

3 SerLeuLeu 5

Db

2 TCTCTCCTC 10

RESULT 182

BQ587767/c

LOCUS

BQ587767 16 bp mRNA linear EST 06-DEC-2002

DEFINITION

E012340w-024-010-M01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA

ACCESSION

BQ587767

VERSION

BQ587767.1 GI:26117349

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

Plant J. 32 (5), 845-857 (2002)

MEDLINE

22362189

PUBMED

12472698

COMMENT

Contact: Weishaar B

FEATURES

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 10 row: M column: 01
Seq primer: SP6; CATACGATTGAGTGACACTATAG.
Location/Qualifiers

source

1..16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="taxon:161934"

/db_xref="GABI:185096"

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/issue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"

/note="Vector: PCWVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"

SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
3.39e+06	3.00	100.00%	100.00%	1.52%	16	3	0	0	0	0

DB:

13

US-09-966-880A-8 (1-198) x BQ587767 (1-16)

QY

24 ArgArgGlu 26

Db

9 AGGAGAGAG 1

RESULT 183

BQ588093

LOCUS

BQ588093 16 bp mRNA linear EST 06-DEC-2002

DEFINITION

E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone

ACCESSION

BQ588093

VERSION

BQ588093.1 GI:26117675

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

REFERENCE

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

Plant J. 32 (5), 845-857 (2002)

MEDLINE

22362189

PUBMED

12472698

COMMENT

Contact: Weishaar B

FEATURES

ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 9 row: A column: 19
Seq primer: SP6; CATACGATTGAGTGACACTATAG.
Location/Qualifiers

source

1..16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db_xref="taxon:161934"

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/issue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"

/note="Vector: PCWVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Bindeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"

SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ588093 (1-16)

QY 22 TysGlyArg 24

DB 4 AAGGAGGA 12

RESULT 184

BQ588093/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

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/db_xref="taxon:161934"

/issue_type="leaf"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6, Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinzamleber Saatzucht AG Bindeck, Germany, contact: b.schulz@kms.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Bet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ588093 (1-16)

QY 42 PheSerLeu 44

DB 13 TTCTCCCTT 5

RESULT 185

BQ588621

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1.16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

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/db_xref="taxon:161934"

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/issue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6, Site 1: SalI, Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinzamleber Saatzucht AG Bindeck, Germany, contact: b.schulz@kms.de; cloning sites SalI-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Bet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.39e+06 Length: 16
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ588621 (1-16)

QY 104 LeuserLeu 106

Db 4 CTTTCTCTC 12

RESULT 186

BQ588621/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. 16

/organism="Beta vulgaris"

/mol_type="mRNA"

/cultivar="KMS2320 (double haploid, monogerm breeding line)"

/db_xref="GABI:187387"

/db_xref="taxon:161934"

/clone="024-015-N03"

/tissue_type="storage root"

/lab_host="EMDH10B"

/clone_lib="MP12-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KMS Kleinwanzlebener Saatgut AG Bindeck, Germany; contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:"

SP6-Sali-CCGCGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 13

US-09-966-880A-8 (1-198) x BQ588621 (1-16)

QY 24 ArgArgGlu 26

Db 16 AGGAGAGAG 8

RESULT 187

CF303743

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 16

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABFL-03-B14"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli SOLR"

/clone_lib="ABFL-overexpressing transgenic rice lambda phage cDNA library (ABFL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Leaf was dried for 2hrs. cDNA was inserted into lambda uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was prepared from ABFL-responsive element binding transcription factor 3 overexpression line."

Alignment Scores:

Pred. No.: 3.39e+06

Score: 3.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 1.52%

DB: 14

US-09-966-880A-8 (1-198) x CF303743 (1-16)

QY 23 G1YArgArg 25

Db 7 GGCGCGCGC 15

RESULT 188

CF306313

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

ABFL-03-B14.g1 ABFL3-overexpressing transgenic rice lambda phage

cDNA library (ABFL) Oryza sativa cDNA clone ABFL-03-B14, mRNA

sequence.

CDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

HDAL-03-G11.g1 HDAL1-overexpressing transgenic rice lambda phage

cDNA library 1 (HAI) Oryza sativa cDNA clone HDAL-03-G11, mRNA

sequence.

CF306313

VERSION

KEYWORDS

EST.

Oryza sativa

16 bp mRNA linear EST 15-AUG-2003

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16
Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDA1-03-G11"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF307345 (1-16)

Oy 38 SerAlaThr 40

Db 10 AGTGCAC 2

RESULT 189

CF307345/c

LOCUS

DEFINITION

CF307345 16 bp mRNA linear EST 15-AUG-2003
HDA1-06-H02.g1 OSHDA1-overexpressing transgenic rice lambda phase
cDNA library I (HDA1) Oryza sativa cDNA clone HDA1-06-H02, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, Greengene Biotech Inc., Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193

Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..16
Location/Qualifiers

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDA1-06-H02"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SOLR"

/clone_lib="OSHDA1-overexpressing transgenic rice lambda phage cDNA library I (HDA1)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; Callus was treated with ABA(20um) for 1hour. cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

ORIGIN

Alignment Scores:

Pred. No.:	3.39e+06	Length:	16
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF307345 (1-16)

Oy 70 LeuAppPro 72

Db 14 TTGATCCT 6

RESULT 190

HSM007757

ID

HSM007757

standard; mRNA; EST; 17 BP.

XX

AC

AL042907,

XX

SV

AL042907.1

XX

DE

Homo sapiens mRNA; EST DKFZp434J1622_r1 (from clone DKFZp434J1622)

XX

KW

EST; expressed sequence tag.

XX

OS

Homo sapiens (human)

XX

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;

XX

OC

Eutheria; Primates; Catarrhini; Homidae; Homo.

XX

XX

[1]

RA

Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;

XX

RL

Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.

XX

CC

MPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY

XX

CC

Clone from S. Wiemann, sequenced by LMU within the cDNA

XX

CC

sequencing consortium of the German Genome Project

XX

CC

No st sequence available

XX

CC

This clone is available at the RZPD in Berlin

XX

CC

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

XX

CC

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX

FH

Key

XX

FH

Location/Qualifiers

XX

FT

source

XX

FT

/db_xref="taxon:9606"

XX

FT

/mol_type="mRNA"

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FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:            2              Gaps:        0

US-09-966-880A-8 (1-198) x HSM007757 (1-17)

QY      79 ThrtTphe 81
Db      3 ACTTGATTC 11

RESULT 191
HSM007757/c
ID      HSM007757      standard; mRNA; EST; 17 BP.
XX
XX      AL042907;
XX
XX      AL042907.1
XX
DT      12-MAR-1999 (Rel. 59, Created)
DT      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434J1622_r1 (from clone DKFZp434J1622)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Euteria; Primates; Catarrhini; Homidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the cDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
FH      1. .17
FT      source
FT      /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 3 A; 2 C; 5 G; 7 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:            2              Gaps:        0

US-09-966-880A-8 (1-198) x HSM007757 (1-17)

QY      193 PheArgThr 195
Db      15 TTCGGAACC 7

RESULT 192
HSM007775/c
ID      HSM007775      standard; mRNA; EST; 17 BP.
XX
XX      AL042925;
XX
XX      AL042925.1
XX
SV      AL042925.1
XX
XX      12-MAR-1999 (Rel. 59, Created)
XX      12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE      Homo sapiens mRNA; EST DKFZp434K1222_r1 (from clone DKFZp434K1222)
XX
XX      EST; expressed sequence tag.
XX
XX      Homo sapiens (human)
XX      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX      Euteria; Primates; Catarrhini; Homidae; Homo.
XX
XX      [1]
XX      Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX      Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX      MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX      Clone from S. Wiemann, sequenced by LMU within the cDNA
XX      sequencing consortium of the German Genome Project
XX      No s1 sequence available
XX      This clone is available at the RZPD in Berlin
XX      Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX      Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX      Key      Location/Qualifiers
FH      1. .17
FT      source
FT      /db_xref="taxon:9606"
FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX

SQ      Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:            2              Gaps:        0

US-09-966-880A-8 (1-198) x HSM007775 (1-17)

QY      193 PheArgThr 195
Db      13 TTCGGAACC 5

RESULT 193

```

AM059592/c 17 bp mRNA linear EST 23-AUG-2000
 LOCUS Hutr.bsc.dnc15.final.cluster_82_(3) DNC15 Homo sapiens cDNA
 DEFINITION Similar to ribosomal protein l12, mRNA sequence.
 ACCESSION AM059592
 VERSION AM059592.1 GI:6651914
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 17)
 Brenner, S., Williams, S.R., Vernaes, E.H., Stork, T., Moon, K.,
 McColium, C., Mao, J.I., Kirchner, J.J., Elet, S., Dubridge, R.B.,
 Burcham, T. and Albrecht, G.
 In vitro cloning of complex mixtures of DNA on microbeads: Physical
 separation of differentially expressed cDNAs
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
 20144098
 MEDLINE 10677516
 COMMENT Contact: Burcham TS
 LYNX Therapeutics, Inc.
 25861 Industrial Blvd., Hayward, CA 94545, USA
 Tel: 510 670 9338
 Fax: 510 670 9302
 Email: timb@lynxgen.com
 Sequence obtained from LYNX Therapeutics Megasort technology.
 Collected from the down-regulated gate. Consensus sequence of 3
 sequences in cluster.
 High quality sequence stop: 17.
 Location/Qualifiers
 1..17
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_type="monocytic leukemia"
 /cell_line="THP-1 (TIB-202)"
 /clone_lib="DNC15"
 /note="Vector: PCR2.1; Cloning of PCR products from
 micro-beads carrying 3' end of down-regulated cDNA. THP-1
 cells non-induced (treated with DMSO only)."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.61e+06 Length: 17
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0
 US-09-966-880A-8 (1-198) x AM059592 (1-17)
 QY 32 ValValLys 34
 |||||
 14 GTTGTCAA 6
 RESULT 194
 AM246528 17 bp mRNA linear EST 07-JAN-2000
 LOCUS 2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
 DEFINITION mRNA sequence.
 ACCESSION AM246528
 VERSION AM246528.1 GI:6589521
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 17)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Other_ESTs: 2821879.5prime
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
 project Clone distribution: MGC clone distribution information can
 be found through the I.M.A.G.E. Consortium/LNL at:
 www.bio.hnl.gov/bdrp/image/image.html Base Calling / Quality
 Scores: PHRED from University of Washington Genome Center
 Trimming: cross match from University of Washington Genome Center
 PHRAP suite, Poly-T identification: patchcut.pl from Berkeley
 Drosophila Genome Project, University of Washington Genome Center:
 http://www.genome.washington.edu Low Quality Sequence: 13
 contiguous PHRED high quality bases following vector sequence. Very
 low quality sequence: Trace file contained 17 contiguous distinct
 peaks following vector sequence. Polyadenylation: Based upon the
 presence of a XhoI site followed by a run of 14 or more T residues
 at the beginning of the sequence, this cDNA insert was
 polyadenylated.
 Plate: LICMT7 row: P column: 8
 High quality sequence stop: 13.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2821879"
 /issue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 7"
 /note="Organ: Lung; Vector: pOT87; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.61e+06 Length: 17
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 10 Gaps: 0
 US-09-966-880A-8 (1-198) x AM246528 (1-17)
 QY 15 PhelyAsn 17
 |||||
 8 TTTAAAC 16
 RESULT 195
 AM246893 17 bp mRNA linear EST 07-JAN-2000
 LOCUS 2822293.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822293 5',
 DEFINITION mRNA sequence.
 ACCESSION AM246893
 VERSION AM246893.1 GI:6589886
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 17)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Other_ESTs: 2822293.3prime

GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com

Seq primer: 17.
Location/Qualifiers

FEATURES

source

1..17
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/ciseue_type="cartilage"
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/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BG926068 (1-17)

QY 169 ServAlarg 171

Db 12 AGTGTGAG 4

RESULT 198

BM395339/C

LOCUS 50072-2-8-F06.r.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM395339

VERSION BM395339.1 GI:18195392

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J., and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

COMMENT Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..17
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00%
Query Match: 1.52%
DB: 12
Gaps: 0

US-09-966-880A-8 (1-198) x BM395339 (1-17)

QY 154 AashAglu 156

Db 14 AATCATGAA 6

RESULT 199

BM396258/C

LOCUS 5009-0-19-G03.t.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM396258

VERSION BM396258.1 GI:18196311

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 17)

AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J., and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

COMMENT Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

FEATURES

source

1..17
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.61e+06	Length:	17
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM396258 (1-17)

QY 77 ArgValThr 79

Db 12 CCGGTGACT 4

RESULT 200

BM401224/C

LOCUS 5009-0-84-D08.t.1 Chilcoat/Turkewitz cDNA (large fraction)

DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM401224

VERSION BM401224.1 GI:18201277

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

```

REFERENCE
AUTHORS      1 (bases 1 to 17)
              Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E.,
              Pranke,J., and Klobutcher,L.
TITLE        EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
              Molecular Genetics and Cell Biology
              University of Chicago
              920 E. 58th Street, Chicago, IL 60637, USA
              Tel: 773 702 4374
              Fax: 773 702 3172
              Email: apturkew@midway.uchicago.edu
              Seq primer: 13.
FEATURES
source       Location/Qualifiers
              1..17
              /organism="Tetrahymena thermophila"
              /mol_type="rRNA"
              /strain="CU428.1"
              /db_xref="taxon:5911"
              /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
              /note="Vector: Bluescript2 SK+; Details on library
              preparation can be found in Chilcoat and Turkewitz (2001)
              Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%        Indels:      0
DB:             12           Gaps:        0
US-09-966-880A-8 (1-198) x BM401224 (1-17)
QY           129 LeuHISArg 131
Db           17 CTCACACGC 9
RESULT 201
LOCUS       BQ587868                      17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION  BQ587868-024-009-024-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION   BQ587868
VERSION     BQ587868.1 GI:26117450
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 17)
REFERENCE   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruick,W., Wenzel,A., O'Brien,J., Lehnach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
TITLE       ADIS DNA core facility at MP1Z
JOURNAL     Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mplz-koeln.mpg.de
            Insert Length: 17 Std Error: 0.00
            Plate: 9 row: 0 column: 24
            Seq primer: SP6; CATACGATTGAGTGACACTATAG.
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mplz-koeln.mpg.de
            Insert Length: 17 Std Error: 0.00
            Plate: 19 row: 0 column: 05
            Seq primer: SP6; CATACGATTGAGTGACACTATAG.
FEATURES
source      Location/Qualifiers
              1..17
              /organism="Beta vulgaris"
              /mol_type="rRNA"
              /cultiivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:184994"
              /db_xref="taxon:161934"
              /clone_lib="MP1Z-ADIS-024-leaf"
              /issue_type="leaf"
              /lab_host="EMDH10B"
              /clone_lib="MP1Z-ADIS-024-leaf"
              /note="Vector: PCWVS-POR6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-SalI-CCACGCGTCCG-5Prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database:http://gabi.rzpd.de"
Alignment Scores:
Pred. No.:      3.61e+06      Length:      17
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    1.52%        Indels:      0
DB:             13           Gaps:        0
US-09-966-880A-8 (1-198) x BQ587868 (1-17)
QY           51 AsnLYGAsn 53
Db           3 AACAAAAC 11
RESULT 202
LOCUS       BQ590447                      17 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION  BQ12839-024-019-005-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
ACCESSION   BQ590447
VERSION     BQ590447.1 GI:26120030
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
            1 (bases 1 to 17)
REFERENCE   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruick,W., Wenzel,A., O'Brien,J., Lehnach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
TITLE       ADIS DNA core facility at MP1Z
JOURNAL     Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mplz-koeln.mpg.de
            Insert Length: 17 Std Error: 0.00
            Plate: 19 row: 0 column: 05
            Seq primer: SP6; CATACGATTGAGTGACACTATAG.
COMMENT     Contact: Weishaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaar@mplz-koeln.mpg.de
            Insert Length: 17 Std Error: 0.00
            Plate: 19 row: 0 column: 05
            Seq primer: SP6; CATACGATTGAGTGACACTATAG.
FEATURES
source      Location/Qualifiers
              1..17
              /organism="Beta vulgaris"
              /mol_type="rRNA"
              /cultiivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:189664"

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/db_xref="taxon:161934"
/clone="024-019-005"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ590447 (1-17)

QY 172 LeuserArg 174
Db 1 CTCTCTCTC 9

RESULT 203
BQ593528 17 bp mRNA linear EST 06-DEC-2002
LOCUS BQ593528
DEFINITION S015525-024-026-123-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593528
VERSION BQ593528.1 GI:26123111
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 17)
Herrig,R., Schulz,B., Weishaar,B., Hennig,S., Steinbach,M.,
Dzurgowski,M., Stahl,D., Wtuck,W., Menze,A., O'Brien,J., Leirach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant T. 32 (5), 845-857 (2002)
22352189
12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 26 row: 1 column: 23
Seg primer: SP6; CATACGATTAGTGACACATATAG.
location/Qualifiers
1..17
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KMS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:193326"
/db_xref="taxon:161934"
/clone="024-026-123"
/tissue_type="developing root"
/lab_host="EMDH10B"

FEATURES
source

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/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ593528 (1-17)

QY 104 LeuserLeu 106
Db 1 CTCTCTCTC 9

RESULT 204
BQ605828 17 bp mRNA linear EST 25-JUN-2002
LOCUS BQ605828
DEFINITION BRY_1399 wheat EST endosperm library Triticum aestivum CDNA 5',
mRNA sequence.
ACCESSION BQ605828
VERSION BQ605828.1 GI:21554934
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 17)
Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences
Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
22478026
12590341
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
location/Qualifiers
1..17
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuana"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN
Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

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US-09-966-880a-8 (1-198) x BQ605828 (1-17)

Qy 56 HisValGlu 58
Db 3 CATGCTCGA 11

RESULT 205

LOCUS BQ605828/c

DEFINITION BQ605828 17 bp mRNA linear EST 25-JUN-2002
BRY 1399 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.

ACCESSION BQ605828
VERSION BQ605828.1 GI:21554934

KEYWORDS EST,
Triticum aestivum (bread wheat)
SOURCE Triticum aestivum

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 17)
Clarke,B., Lambrecht,M. and Rhee,S.Y.
Arabidopsis genomic information for interpreting wheat EST
sequences

REFERENCE
AUTHORS
TITLE

JOURNAL Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE 22478026
PubMed 12590341

COMMENT Contact: Lambrecht M

The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhees@cma.stanford.edu.

FEATURES
Location/Qualifiers

1..17
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Myuna"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN

Alignment Scores:

Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ605828 (1-17)

Qy 105 SerLeuArg 107
Db 15 TCGCTTGA 7

RESULT 206

LOCUS CF299737

DEFINITION 7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-N22, mRNA sequence.

ACCESSION CF299737
VERSION CF299737.1 GI:33671498

KEYWORDS EST,
Oryza sativa
SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 17)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-N22"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site: 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF299737 (1-17)

Qy 25 ArgGluThr 27
Db 2 CCGGAACA 10

RESULT 207

LOCUS CF299737/c

DEFINITION 7LEAF--03-N22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-N22, mRNA sequence.

ACCESSION CF299737
VERSION CF299737.1 GI:33671498

KEYWORDS EST,
Oryza sativa
SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzae; Oryza.
1 (bases 1 to 17)

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"

ACCESSION CF921142
 VERSION CF921142.1 GI:38191936
 KEYWORDS
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustoside I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 REFERENCE 1 (bases 1 to 17)
 Schaeffer, B.E., Huang, S., Liu, X., Nguyen, H., Duke, M. and Stacey, G.
 Expressed sequence tags from soybean root hair subtractive cDNA library
 JOURNAL Unpublished (2003)
 COMMENT Contact: Gary Stacey
 University of Missouri
 108 Waters Hall, Columbia, MO 65211, USA
 Tel: 573-884-4752
 Fax: 573-882-0588
 Email: stacey@missouri.edu
 Single pass sequence
 Seq primer: 17
 FEATURES
 source
 Location/Qualifiers
 1..17
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams 82"
 /db_xref="taxon:3847"
 /tissue_type="root hairs"
 /clone_lib="Soybean root hair subtracted cDNA library gmrhwm3"
 /note="Organ: root hairs; Vector: PCR2-1 Topo; cDNA clones generated from soybean root hair tissue treated with Brachytrichobium japonicum for 3 hours."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.61e+06 Length: 17
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x CF921142 (1-17)
 QY 31 TTTTAAAT 33
 DB 17 TATGTTGTA 9
 RESULT 211
 D11808/c 17 bp mRNA linear EST 02-DEC-1992
 LOCUS HUMMO1H11 Liver HepG2 cell line. Homo sapiens cDNA clone hm01h11,
 DEFINITION mRNA sequence.
 ACCESSION D11808
 VERSION D11808.1 GI:2155083
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 17)
 Okubo, K., Hori, N., Matoba, R., Niiyama, T., Fukushima, A., Kojima, Y. and Matsubara, K.
 Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
 JOURNAL Nat. Genet. 2, 173-179 (1992)
 MEDLINE 94258199
 COMMENT Contact: Kouzaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki Niiyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara
 Institute for Molecular and Cellular Biology

Osaka University
 1-3 Yamada-oka, Suita, Osaka 565, Japan.
 FEATURES
 Location/Qualifiers
 1..17
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:D088354E"
 /db_xref="taxon:9606"
 /clone="hm01h11"
 /lab_host="E.coli"
 /clone_lib="Liver HepG2 cell line."
 /note="3'-directed regional cDNA library. Cleaved by MboI and transformed into E.coli."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.61e+06 Length: 17
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0
 US-09-966-880A-8 (1-198) x D11808 (1-17)
 QY 185 GTTAAAT 187
 DB 14 GAGGTCGAT 6
 RESULT 212
 PCH303755 17 bp DNA linear GSS 03-APR-2001
 LOCUS Plasmodium chabaudi genome survey sequence, clone PCT05.plt,
 DEFINITION genomic survey sequence.
 ACCESSION AJ303755
 VERSION AJ303755.1 GI:11140262
 KEYWORDS GSS; genome survey sequence.
 SOURCE Plasmodium chabaudi
 ORGANISM Plasmodium chabaudi
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 17)
 Janssen, C.S., Barrett, M.P., Lawson, D., Quail, M.A., Harris, D., Bowman, S., Phillips, R.S. and Turner, C.M.
 Gene discovery in Plasmodium chabaudi by genome survey sequencing
 JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
 MEDLINE 11295179
 PUBLISHED 21192558
 REFERENCE 2 (bases 1 to 17)
 Janssen, C.S.
 DIRECT SUBMISSION
 Submitted (06-NOV-2000) Division of Infection & Immunity,
 University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
 COMMENT bases 39 to 55 (OL to SR).
 FEATURES
 source
 Location/Qualifiers
 1..17
 /organism="Plasmodium chabaudi"
 /mol_type="genomic DNA"
 /db_xref="taxon:5825"
 /clone="PCT05.plt"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.61e+06 Length: 17
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 29 Gaps: 0
 US-09-966-880A-8 (1-198) x PCH303755 (1-17)
 QY 113 LNTTTPPHE 115
 DB 113 LNTTTPPHE 115

Db 3 CTGTATTTT 11

RESULT 213
PCH303755/C
LOCUS PCH303755/C
DEFINITION Plasmodium chabaudi genome survey sequence, clone PCTc5.plt.
ACCESSION AJ303755
VERSION AJ303755.1 GI:11140262
KEYWORDS GSS; genome survey sequence.
SOURCE Plasmodium chabaudi
ORGANISM Plasmodium chabaudi
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 17)
AUTHORS Janssen,C.S., Barrett,M.P., Lawson,D., Quail,M.A., Harris,D.,
Bowman,S., Phillips,R.S. and Turner,C.M.
TITLE Gene discovery in Plasmodium chabaudi by genome survey sequencing
JOURNAL Mol. Biochem. Parasitol. 113 (2), 251-260 (2001)
MEDLINE 21125358
PUBMED 11295179
REFERENCE 2 (bases 1 to 17)
AUTHORS Janssen,C.S.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2000) Division of Infection & Immunity,
University of Glasgow, Joseph Black Building, Glasgow G12 8QQ, UK
COMMENT bases 39 to 55 (OL to SR).
FEATURES
source 1..17
location/Qualifiers
1..17
/organism="Plasmodium chabaudi"
/mol_type="genomic DNA"
/db_xref="taxon:5825"
/clone="PCTc5.plt"

ORIGIN

Alignment Scores:
Pred. No.: 3.61e+06 Length: 17
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x PCH303755, (1-17)

QY 15 PheLysAsn 17
Db 15 TTTAAAT 7

RESULT 214
HSM004368/C
ID HSM004368 standard; mRNA; EST, 18 BP.
XX
AC AL039892;
XX
SV AL039892.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434G1212_r1 (from clone DKFZp434G1212)
XX
XX EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
RN [1]
RP 1-18
RA Duesterhoeft A., Lauber J., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Kiopterapitz 18a D-82152 Martinsried, GERMANY

XX
CC Clone from S. Wiemann, sequenced by Qiagen within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..18
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone="DKFZp434G1212"
FT /clone_1ib="434 (synonym: hres3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
FT
XX

Sequence 18 BP; 3 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x HSM004368 (1-18)

QY 193 PheArgThr 195
Db 14 TTCGGACC 6

RESULT 215
HSM007922/C
ID HSM007922 standard; mRNA; EST, 18 BP.
XX
AC AL043072;
XX
SV AL043072.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434B1823_r1 (from clone DKFZp434B1823)
XX
XX EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
XX
RN [1]
RP 1-18
RA Blum H., Buererachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Kiopterapitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1..18
FT /db_xref="taxon:9606"

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FT      /mol_type="mRNA"
FT      /organism="Homo sapiens"
FT      /clone_id="DKFZp434B1.823"
FT      /clone_1ib="434 (synonym: htes3). Vector pSport1; host
FT      DH10B; sites NotI + SalI"
FT      /dev_stage="adult"
FT      /tissue_type="testis"
XX
SQ      Sequence 18 bp; 3 A; 6 C; 5 G; 4 T; 0 other;

Alignment Scores:
Pred. No.:      3.83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             2            Gaps:        0

US-09-966-880A-8 (1-198) x HSM007922 (1-18)

Qy      193 PheArgThr 195
Db      16 TTCCCGACC 8

RESULT 216
LOCUS      AM246505      18 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821585.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821585 3',
ACCESSION      AM246505
VERSION      AM246505.1 GI:6589498
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821585.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: DCTD/DMP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 18
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: trace file contained 18 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: L10M7 row: D column: 2
High quality sequence stop: 18.
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821585"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7, Site_1: XhoI; Site_2:

```

```

ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.:      3.83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    1.52%          Indels:      0
DB:             10            Gaps:        0

US-09-966-880A-8 (1-198) x AM246505 (1-18)

Qy      42 PheSerLeu 44
Db      7 TTTCTTTA 15

RESULT 217
LOCUS      AM250267      18 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION      2821151.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821151 5',
ACCESSION      AM250267
VERSION      AM250267.1 GI:6593260
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 18)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821151.3prime
Contact: Robert Strausberg, Ph.D.
Email: cgaabbs-remail.nih.gov
Tissue Procurement: DCTD/DMP CDNA Library Preparation: Ling
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
Project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 16
contiguous PHRED high quality bases following vector sequence. Very
low Quality Sequence: trace file contained 18 contiguous distinct
peaks following vector sequence.
Plate: L10M6 row: A column: 24
High quality sequence stop: 16.
Location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821151"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7, Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

```

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ALIGNMENT SCORES:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AW250267 (1-18)

QY 23 G1YATGATG 25
DB 9 GGGAGGCGG 17

RESULT 218

AW250449 18 bp mRNA linear EST 07-JAN-2000
LOCUS 2822458.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822458 3',
DEFINITION mRNA sequence.

ACCESSION AW250449

VERSION AW250449.1 GI:6593442

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS NIH-MGC <http://mgi.mci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2822458.3prime

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing

Project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LNL at:

<http://www.bic.lnhl.gov/bicrp/image/image.html> Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

<http://www.genome.washington.edu> Low Quality Sequence: 18

contiguous PHRED high quality bases following vector sequence. Very

low Quality Sequence: Trace file contained 18 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was

polyadenylated.

Plate: LTCM9 row: H column: 11

High quality sequence stop: 18.

Location/Qualifiers

FEATURES

source

1..18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2822458"

/tissue_type="small cell carcinoma"

/cell_line="MGC3"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_7"

/note="Organ: Lung; Vector: pOTB7; Site 1: XhoI; Site 2:

ScorI; cDNA made by oligo-dt priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAAGAG(G) Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

ALIGNMENT SCORES:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	10	Gaps:	0

US-09-966-880A-8 (1-198) x AW250449 (1-18)

QY 42 PhSeSerLeu 44
DB 7 TTTTCCCTT 15

RESULT 219

BG668027 18 bp mRNA linear EST 30-APR-2001
LOCUS DRABTE12 Rat DRG Library Rattus norvegicus cDNA clone DRABTE12 5',
DEFINITION mRNA sequence.

ACCESSION BG668027

VERSION BG668027.1 GI:13889949

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;

Rattus.

REFERENCE 1 (bases 1 to 18)

AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,

Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,

Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

Identification of gene expression profile of dorsal root ganglion

in the rat peripheral axotomy model of neuropathic pain

Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

JOURNAL MEDLINE

PUBMED 12060780

COMMENT Contact: Zhang Xu

Laboratory of Sensory System

Institute of Neuroscience

320 Yue Yang Road, Shanghai 200031, P.R.China

Tel: 86-21-64748700-121

Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome

Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,

Pudong New Area, P.R.China. Please contact with Zhang Xu

(xu.zhang@ion.ac.cn) or Han Zeguang (hanzeg@chgc.sh.cn)

PCR Primers

FORWARD: T3

BACKWARD: T7

Seq primer: T3

POLYA=No.

Location/Qualifiers

1..18

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="DRABTE12"

/sex="male"

/tissue_type="dorsal root ganglion"

/dev_stage="adult"

/clone_lib="Rat DRG Library"

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG668027 (1-18)

Qy 41 Serpineser 43
17 TCTTCTCC 9

RESULT 220

LOCUS BG668047

DEFINITION DRABUA12 Rat DRG Library Rattus norvegicus cDNA clone DRABUA12 5', mRNA sequence.

ACCESSION BG668047

VERSION BG668047.1 GI:13889969

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 18)

Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C.,

Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D.,

Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.

Identification of gene expression profile of dorsal root ganglion

in the rat peripheral axotomy model of neuropathic pain

Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

JOURNAL MEDLINE

PUBMED 22056133

COMMENT 12060780

Contact: Zhang Xu

Laboratory of Sensory System

Institute of Neuroscience

320 Yue Yang Road, Shanghai 200031, P.R. China

Tel: 86-21-64748700-121

Fax: 86-21-64713446

Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome

Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,

Pudong New Area, P.R.China. Please contact with Zhang Xu

(xu.zhang@ion.ac.cn) or Han Zeguang (hanzegu@sh.sh.cn)

PCR Primers

FORWARD: T3

BACKWARD: T7

Seq primer: T3

POLYA=No.

FEATURES Location/Qualifiers

1..18 /organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="DRABUA12"

/sex="male"

/tissue_type="dorsal root ganglion"

/dev_stage="adult"

/clone_lib="Rat DRG Library"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG668047 (1-18)

Qy 104 LeuSerLeu 106

|||||

DB 2 CTCCTCTC 10

RESULT 221

LOCUS BG896958

DEFINITION HOA59-1-D4.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG896958

VERSION BG896958.1 GI:14307199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 18)

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

Lark, M.W.

Identification and initial characterization of 5000 expressed

sequenced tags (ESTs) each from adult human normal and

osteoarthritic cartilage cDNA libraries

Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE

PUBMED 21482651

COMMENT 11597177

Contact: Sanjay Kumar

UW2109

GlaxoSmithKline

709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA

Tel: 610-270-7245

Fax: 610-270-5598

Email: sanjay.kumar-1@gsk.com

Seq primer: T7

Location/Qualifiers

1..18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="cartilage"

/lab_host="E.coli DH10 B"

/clone_lib="HOA (Human Osteoarthritic Cartilage)"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;

Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG896958 (1-18)

Qy 180 LeuLeuPro 182

DB 4 CTCCTCCC 12

RESULT 222

LOCUS BG896958/c

DEFINITION HOA59-1-D4.R HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA, mRNA sequence.

ACCESSION BG896958

VERSION BG896958.1 GI:14307199

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 18)

Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,

Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and

REFERENCE

AUTHORS

TITLE Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthritis. Cartil. 9 (7), 641-655 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: T7,
Location/Qualifiers

FEATURES
source 1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG900971 (1-18)

QY 23 GYARGATG 25
DB 11 GGAGAGAGG 3

RESULT 223

LOCUS BG900971 18 bp mRNA linear EST 06-NOV-2001
DEFINITION HOA52-1-C2.R HOA (Human Osteoarthritic Cartilage) Homo sapiens
CDNA, mRNA sequence.
ACCESSION BG900971
VERSION BG900971.1 GI:14311220
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
AUTHORS Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthritis. Cartil. 9 (7), 641-655 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: T7,
Location/Qualifiers

FEATURES
source 1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

ORIGIN
Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG900971 (1-18)

QY 105 SerLeuArg 107
DB 5 TCCTTAGC 13

RESULT 224

LOCUS BG924473 18 bp mRNA linear EST 06-NOV-2001
DEFINITION HNC27-1-D2.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA
sequence.
ACCESSION BG924473
VERSION BG924473.1 GI:14318996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
AUTHORS Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL Osteoarthritis. Cartil. 9 (7), 641-655 (2001)
MEDLINE 21482651
PUBMED 11597177
COMMENT Contact: Sanjay Kumar
UM2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@sk.com
Seq primer: T7,
Location/Qualifiers

FEATURES
source 1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN
Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG924473 (1-18)

QY 112 ArgLeuTyr 114
Db 2 AGACTCTAT 10

RESULT 225 BG924473 18 bp mRNA linear EST 06-NOV-2001
LOCUS BG924473/c HNC27-1-D2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.

ACCESSION BG924473
VERSION BG924473.1 GI:14318996
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 18)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651
PubMed 11597177
COMMENT Contact: Sanjay Kumar
UW2109
GlaxoSmithKline
709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.

FEATURES
source location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG924473 (1-18)

QY 76 TyrArgVal 78
Db 11 TATAGAGTC 3

RESULT 226 BG925410 18 bp mRNA linear EST 06-NOV-2001
LOCUS BG925410 HNC5-1-B6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG925410
VERSION BG925410.1 GI:14319933
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 18)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651
PubMed 11597177
COMMENT Contact: Sanjay Kumar
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Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay.kumar-1@gsk.com
Seq primer: T7.

FEATURES

source location/Qualifiers
1..18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI; Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880a-8 (1-198) x BG925410 (1-18)

QY 104 LeuSerLeu 106
Db 4 CTCTCCCTA 12

RESULT 227 BG925569 18 bp mRNA linear EST 06-NOV-2001
LOCUS BG925569 HNC5-1-B2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG925569
VERSION BG925569.1 GI:14320092
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 18)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
Osteoarthr. Cartil. 9 (7), 641-653 (2001)

JOURNAL MEDLINE 21482651
PubMed 11597177
COMMENT Contact: Sanjay Kumar
UW2109
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709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245

Fax: 610-270-5598
Email: sanjay_kumar-1@gsf.com
Seq primer: T7,
Location/Qualifiers

FEATURES
source
1..18

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/feature_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925569 (1-18)

QY 181 LeuProLeu 183

Db 4 CTCCTCCTC 12

RESULT 228
LOCUS BG925569/c 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC5-1-E2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BG925569.1 GI:14320092

VERSION BG925569.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.

AUTHORS Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries

TITLE

JOURNAL
MEDLINE 21482651 (2001)
PUBMED 11597177

COMMENT Contact: Sanjay Kumar

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GlaxoSmithKline
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Fax: 610-270-5598

Email: sanjay_kumar-1@gsf.com

Seq primer: T7,
Location/Qualifiers

FEATURES
source
1..18

/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/feature_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18

Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG925569 (1-18)

QY 24 ArgArgGlu 26

Db 18 AGAGAGGAG 10

RESULT 229

BG927414

LOCUS BG927414 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BG927414.1 GI:14321937

VERSION BG927414.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathre,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.

AUTHORS Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries

TITLE

JOURNAL
MEDLINE 21482651 (2001)
PUBMED 11597177

COMMENT Contact: Sanjay Kumar

UN2109

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Fax: 610-270-5598

Email: sanjay_kumar-1@gsf.com

Seq primer: T7,
Location/Qualifiers

FEATURES
source
1..18

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/feature_type="cartilage"

/lab_host="E.coli DH10 B"

/clone_lib="HNC (Human Normal Cartilage)"

/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BG927414 (1-18)

QY 59 LeuLeuPhe 61

Db 2 CTCCTCCTC 10

RESULT 230

BG927414/c

LOCUS BG927414 18 bp mRNA linear EST 06-NOV-2001

DEFINITION HNC1-1-H3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.

ACCESSION BG927414 GI:14321937
 VERSION BG927414.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 18)
 Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathie,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Larr,M.W.
 Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)
 JOURNAL MEDLINE PUBMED
 21482651
 11597177
 CONTACT: Sanjay Kumar
 UW2109
 GlaxoSmithKline
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 Tel: 610-270-7245
 Fax: 610-270-5598
 Email: sanjay.kumar-1@sk.com
 Seq primer: T7
 FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="Cartilage"
 /lab_host="E.coli DH10 B"
 /clone_lib="VNC (Human Normal Cartilage)"
 /note="Vector: pSPORT 1; Site_1: Salt; Site_2: Not; Directional"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0
 US-09-966-880A-8 (1-198) x BG927414 (1-18)
 QY 24 ArgArgGlu 26
 |||||
 11 AGAAGAGAA 3
 RESULT 231
 BM394601 18 bp mRNA linear EST 17-JAN-2002
 50072-2-4-H10.r.1 Chiloat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM394601
 VERSION BM394601.1 GI:18194654
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 18)
 Turkewitz,A.P., Karer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 TITLE JOURNAL
 COMMENT
 DB: 12 Gaps: 0

Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chiloat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chiloat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0
 US-09-966-880A-8 (1-198) x BM394601 (1-18)
 QY 177 ArgArgile 179
 |||||
 2 CGCCGTATA 10
 RESULT 232
 BM394638 18 bp mRNA linear EST 17-JAN-2002
 50072-2-5-B10.r.1 Chiloat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM394638
 VERSION BM394638.1 GI:18194691
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 18)
 Turkewitz,A.P., Karer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 FEATURES
 source
 1..18
 Location/Qualifiers
 /organism="Tetrahymena thermophila"
 /mol_type="mRNA"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chiloat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chiloat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM394638 (1-18)

Qy 129 LeuHISArg 131
18 CTCGACCGC 10

RESULT 233

BM395123

DEFINITION 50072-2-7-F05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM395123

VERSION

BM395123.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

source

Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM395123 (1-18)

Qy 19 ArgTPALA 21
2 CGATGGGCT 10

RESULT 234

BM397227

DEFINITION 5009-0-3-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397227

VERSION

BM397227.1

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE
AUTHORS
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)
Turkewitz, A.P., Karer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.

TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

source

Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 12 Gaps: 0

US-09-966-880A-8 (1-198) x BM397227 (1-18)

Qy 77 ArgValThr 79
10 CGCGTACT 2

RESULT 235

BM397853

DEFINITION 5009-0-38-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION

BM397853

VERSION

BM397853.1

KEYWORDS

EST.

SOURCE

ORGANISM

Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)
Turkewitz, A.P., Karer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
Frankel, J. and Klobutcher, L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES

source

Location/Qualifiers
1..18
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_1ib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

FEATURES	source	1.18
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	
JOURNAL	EST from Tetrahymena thermophila, strain CU428.1, growing cells	
COMMENT	Contact: Turkewitz AP	
Unpublished (2002)		
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	1.52%	
DB:	12	
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	
JOURNAL	EST from Tetrahymena thermophila, strain CU428.1, growing cells	
COMMENT	Contact: Turkewitz AP	
Unpublished (2002)		
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	1.52%	
DB:	12	
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	
JOURNAL	EST from Tetrahymena thermophila, strain CU428.1, growing cells	
COMMENT	Contact: Turkewitz AP	
Unpublished (2002)		
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	1.52%	
DB:	12	
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	
JOURNAL	EST from Tetrahymena thermophila, strain CU428.1, growing cells	
COMMENT	Contact: Turkewitz AP	
Unpublished (2002)		
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	1.52%	
DB:	12	
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	
JOURNAL	EST from Tetrahymena thermophila, strain CU428.1, growing cells	
COMMENT	Contact: Turkewitz AP	
Unpublished (2002)		
Percent Similarity:	100.00%	
Best Local Similarity:	100.00%	
Query Match:	1.52%	
DB:	12	
US-09-966-880A-8 (1-198) x BM398577 (1-18)		
QY	120	122
DB	2	10
RESULT 238		
LOCUS	BM401236	
DEFINITION	5009-0-84-B12.t.1 Chiloat/Turkewitz cDNA (large fraction)	
ACCESSION	Tetrahymena thermophila cDNA, mRNA sequence.	
VERSION	BM401236	
KEYWORDS	EST.	
SOURCE	Unpublished (2002)	
ORGANISM	Tetrahymena thermophila	
REFERENCE	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymena; Tetrahymena.	
AUTHORS	1 (bases 1 to 18)	
TITLE	Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.	

/db_xref="taxon:5911"
 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM401236 (1-18)

QY 77 Argvalthr 79

DB 3 CCGATCAGC 11

RESULT 239

BM401236/c 18 bp mRNA linear EST 17-JAN-2002

DEFINITION 5009-0-84-B12.c.1 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM401236

VERSION BM401236.1 GI:18201289

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

REFERENCE 1 (bases 1 to 18)

AUTHORS Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E.,

Frankel,J. and Klobutcher,L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

COMMENT Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3

FEATURES

Location/Qualifiers

1..18

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript SK+; Details on library

preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM401236 (1-18)

QY 77 Argvalthr 79

DB 13 CCGGTGACT 5

RESULT 240

BM675715/c
 LOCUS BM675715 18 bp mRNA linear EST 27-FEB-2002
 DEFINITION TOH6026767971.R1 CSECFX135 adipose Sus scrofa cDNA, mRNA sequence.
 ACCESSION BM675715
 VERSION BM675715.1 GI:18985613
 KEYWORDS EST.

ORIGIN

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	12	Gaps:	0

US-09-966-880A-8 (1-198) x BM675715 (1-18)

QY 129 LeuHisArg 131

DB 16 CTCACCGC 8

RESULT 241

BM675715/c 18 bp mRNA linear EST 06-DEC-2002

DEFINITION E011887-024-004-L12-SP6 MP12-ADIS-024-inflorescence Beta vulgaris

ACCESSION BM675715

VERSION BM675715.1 GI:26113417

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 18)

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,

Drumowski,M., Stahl,D., Wronck,W., Menze,A., O'Brien,J., Lehnach,H.

and Radehof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472696

TITLE

JOURNAL

MEDLINE

PUBMED

12472696

12472696

12472696

12472696

12472696

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaamp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
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Seq primer: SP6; CATACATTGAGTGAAGACTATAG.

FEATURES

source

Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182866"
/db_xref="taxon:161934"
/clone="024-004-E12"
/tissue_type="inflorescence"
/lab_host="EMD108"
/clone_id="MP1Z-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzlebener SaatZucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ583840 (1-18)

Cy 59 LeuLeupne 61
|||||
6 CTGCTCTTT 14

RESULT 242

BQ584794

LOCUS

DEFINITION E011673-024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION BQ584794.1 GI:26114371

VERSION BQ584794.1

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 18)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelet,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany

FEATURES

source

Fax: 00492215062851
Email: weisshaamp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 2 row: E column: 13
Seq primer: SP6; ATTAGGTGACACTATAGAGA.
Location/Qualifiers
1..18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:181907"
/db_xref="taxon:161934"
/clone="024-002-E13"
/tissue_type="inflorescence"
/lab_host="EMD108"
/clone_id="MP1Z-ADIS-024-inflorescence"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleimanzlebener SaatZucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ584794 (1-18)

Cy 196 LeuGlyLeu 198
|||||
10 TTGGGCTTG 18

RESULT 243

BQ584794/c

LOCUS

DEFINITION E011673-024-002-E13-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION BQ584794.1 GI:26114371

VERSION BQ584794.1

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 18)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfach,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelet,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE

PUBMED

COMMENT

Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaamp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 2 row: E column: 13

FEATURES
Seq primer: SP6; ATTAGTGACACTATAGAGA.
Location/Qualifiers

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/db_xref="taxon:161934"
/clone="024-002-El3"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatnucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
```

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ584794 (1-18)

QY 101 AsnpProasn 103
|||||

Db 17 AACCCCAT 9

RESULT 244

BQ586069 18 bp mRNA linear EST 06-DEC-2002
LOCUS E013394-024-013-B09-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-013-B09 5-PRIME, mRNA sequence.

ACCESSION BQ586069
VERSION BQ586069.1 GI:26115651
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radclouf,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 13 row: B column: 09
Seq primer: SP6; CATCGATTAGTGACACTATAG.
Location/Qualifiers

FEATURES
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/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatnucht AG Binbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polYA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
```

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 13 Gaps: 0

US-09-966-880a-8 (1-198) x BQ586069 (1-18)

QY 52 LysAsnGly 54
|||||

Db 9 AAAATGGA 17

RESULT 245

BQ586393 18 bp mRNA linear EST 06-DEC-2002
LOCUS S014468-024-013-P11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-013-P11 5-PRIME, mRNA sequence.

ACCESSION BQ586393
VERSION BQ586393.1 GI:26115965
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 18)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfach,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radclouf,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
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Location/Qualifiers

FEATURES
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/db_xref="GABI:186486"


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/db_xref="taxon:161934"
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/notes="Vector: PCWVS-P016; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kms.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

```

ORIGIN

Alignment Scores:

Pred. No.:	3	83e+06	Length:	18
Score:	3.00	Matches:	3	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	1.52%	Indels:	0	
DB:	13	Gaps:	0	

US-09-966-880A-8 (1-198) x BQ586393 (1-18)

Qy 107 Argillephe 109

Db 1 CGTATCTTC 9

RESULT 246

BQ586393/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

```

BQ586393 18 bp mRNA linear EST 06-DEC-2002
S014468-024-013-P11-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
024-013-P11 5-PRIME, mRNA sequence.
BQ586393
BQ586393.1 GI:26115965
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 13 row: P column: 11
Seq primer: SP6; CATACGATTGAGTGCACACTATAG.
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/lab_host="EMDH10B"

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/clone_lib="MP1Z-ADIS-024-leaf"
/notes="Vector: PCWVS-P016; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulz@kms.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCAGCGGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-BEET
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

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ORIGIN

Alignment Scores:

Pred. No.:	3	83e+06	Length:	18
Score:	3.00	Matches:	3	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	1.52%	Indels:	0	
DB:	13	Gaps:	0	

US-09-966-880A-8 (1-198) x BQ586393 (1-18)

Qy 22 LysGlyArg 24

Db 13 AACGGAAGA 5

RESULT 247

BQ589347

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

```

BQ589347 18 bp mRNA linear EST 06-DEC-2002
S014007-024-015-A02-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-015-A02 5-PRIME, mRNA sequence.
BQ589347
BQ589347.1 GI:26118930
EST.
Beta vulgaris
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 18)
Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mp1z-koeln.mpg.de
Insert Length: 18 Std Error: 0.00
Plate: 15 row: A column: 02
Seq primer: SP6; CATACGATTGAGTGCACACTATAG.
Location/Qualifiers
1..18
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/cultivar="KMS2320 (double haploid, monogerm breeding
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/db_xref="GABI:187726"
/db_xref="taxon:161934"
/clone="024-015-A02"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/notes="Vector: PCWVS-P016; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KMS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:

```

ORIGIN
 Alignment Scores:
 Pred. No.: 3 83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN
 Alignment Scores:
 Pred. No.: 3 83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Qy 58 GluLeuLeu 60
 Db 2 GAATTA 10

RESULT 248
 BQ591606 18 bp mRNA linear EST 06-DEC-2002
 LOCUS E012442-024-017-G11-SP6 MP12-ADIS-024-developing root Beta vulgaris
 DEFINITION CDNA clone 024-017-G11 5-PRIME, mRNA sequence.
 BQ591606
 ACCESSION BQ591606.1 GI:26121189
 VERSION EST.
 KEYWORDS Beta vulgaris
 SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 18)
 Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wuck, M., Menze, A., O'Brien, J., Leinrich, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 CONTACT: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 Insert Length: 18 Std Error: 0.00
 Plate: 17 row: G column: 11
 Seq primer: SP6; CATACGATTAGGTCACACTATAG.
 Location/Qualifiers
 1..18

FEATURES
 source
 /organism="Beta vulgaris"
 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:188509"
 /db_xref="taxon:161934"
 /clone="024-017-G11"
 /tissue_type="storage root"
 /lab_host="EMDH108"
 /clone_1ib="MP12-ADIS-024-storage root"
 /note="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatgut AG Bindeck, Germany; contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet

ORIGIN
 Alignment Scores:
 Pred. No.: 3 83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

ORIGIN
 Alignment Scores:
 Pred. No.: 3 83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Qy 42 PheSerLeu 44
 Db 4 TTTCACCT 12

RESULT 249
 BQ594437 18 bp mRNA linear EST 06-DEC-2002
 LOCUS E012442-024-024-M20-SP6 MP12-ADIS-024-developing root Beta vulgaris
 DEFINITION CDNA clone 024-024-M20 5-PRIME, mRNA sequence.
 BQ594437
 ACCESSION BQ594437.1 GI:26124020
 VERSION EST.
 KEYWORDS Beta vulgaris
 SOURCE Beta vulgaris
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 18)
 Hwang, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
 Drungowski, M., Stahl, D., Wuck, M., Menze, A., O'Brien, J., Leinrich, H.
 and Radelof, U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 CONTACT: Weishaar B
 ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 Insert Length: 18 Std Error: 0.00
 Plate: 24 row: M column: 20
 Seq primer: SP6; CATACGATTAGGTCACACTATAG.
 Location/Qualifiers
 1..18

FEATURES
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 /mol_type="mRNA"
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"
 /db_xref="GABI:192416"
 /db_xref="taxon:161934"
 /clone="024-024-M20"
 /tissue_type="developing root"
 /lab_host="EMDH108"
 /clone_1ib="MP12-ADIS-024-developing root"
 /note="vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KWS
 Kleinwanzlebener Saatgut AG Bindeck, Germany; contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet

ORIGIN
 Alignment Scores:
 Pred. No.: 3 83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x BQ591606 (1-18)

Project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x BQ594437 (1-18)

QY 104 Leusertleu 106
18 CTCCTCTCTA 10

RESULT 250
BQ790001 18 bp mRNA linear EST 30-JUL-2002

LOCUS
BQ790001
DEFINITION
hage005aH02 Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion annosum cDNA clone hage005aH02, mRNA sequence.

ACCESSION
BQ790001
VERSION
BQ790001.1 GI:22004963

KEYWORDS
EST.

SOURCE
Pinus sylvestris/Heterobasidion annosum

ORGANISM
Pinus sylvestris/Heterobasidion annosum

REFERENCE
1 (bases 1 to 18)
Asiegbu, F.O., Nahalkova, J. and Dean, R.A.
Selected Expressed sequence tags of cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)

AUTHORS
Unpublished (2001)

JOURNAL
Contract: Fred O. Asiegbu

COMMENT
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026, S-750 07, Uppsala, Sweden
Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@koptat.slu.se
Seq primer: 17 primer.
Location/Qualifiers
1. 18
/organism="Pinus sylvestris/Heterobasidion annosum"
/mol_type="mRNA"
/db_xref="taxon:169015"
/clone="hage005aH02"
/dev_stage="Seedling roots of scots pine were infected for 6 days with H. annosum"
/clone_lib="Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library"
/note="Vector: pT-Adv; Site: 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidion annosum (Fps)."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x BQ790001 (1-18)

QY 58 Glueuleu 60
6 GAGCTGCTC 14

RESULT 251
C00629

LOCUS
C00629 18 bp mRNA linear EST 31-DEC-2002
HUMGS0008172 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.

ACCESSION
C00629
VERSION
C00629.1 GI:1432859

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 18)
Okubo, K.
BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111 (ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

AUTHORS
Unpublished (1995)

JOURNAL
Contact: Okubo, K.

COMMENT
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111 (ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ

FEATURES
Location/Qualifiers
1. 18
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x C00629 (1-18)

QY 179 Iileuleu 181
2 ATCTGCTG 10

RESULT 252
C01086 18 bp mRNA linear EST 31-DEC-2002
C01086/c
LOCUS
HUMGS0007743 Human adult (K.Okubo) Homo sapiens cDNA, mRNA sequence.

ACCESSION
C01086
VERSION
C01086.1 GI:1433316

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 18)
Okubo, K.
BodyMap: human gene expression database
Unpublished (1995)
Contact: Okubo, K.
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111 (ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ

AUTHORS
Unpublished (1995)

JOURNAL
Contact: Okubo, K.

COMMENT
Institute for Molecular and Cellular Biol
Osaka University
1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111 (ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DBJ

since 1993. For the abundance information of clones with this sequence in this library and as well as in other 3'-directed libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The sequences of the clones represented by this GS sequences is also found there.

FEATURES

source

1..18
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Human adult (K.Okubo)"
/note="One or more human adult tissue"

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x C01086 (1-18)

Qy 32 ValValVal 34

Db 14 GTTGTCAAA 6

RESULT 253

C20904 18 bp mRNA linear EST 31-DEC-2002
LOCUS HUMGS0004983 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION sequence.

ACCESSION C20904.1 GI:1622014

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)

AUTHORS Okubo,K.

TITLE BodyMap: human gene expression database

JOURNAL Unpublished (1995)

COMMENT Contact: Okubo,K.

Institute for Molecular and Cellular Biol

Osaka University

1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111(ex.3315)

Email: kouzak@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DBJ

since 1993. For the abundance information of clones with this

sequence in this library and as well as in other 3'-directed

libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The

sequences of the clones represented by this GS sequences is also

found there.

Location/Qualifiers

1..18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="adult"

/clone_lib="Human adult (K.Okubo)"

/note="One or more human adult tissue"

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0

DB: 13 Gaps: 0

US-09-966-880A-8 (1-198) x C20904 (1-18)

Qy 178 ArgileLeu 180

Db 5 AGGATCTC 13

RESULT 254

C21336 18 bp mRNA linear EST 31-DEC-2002
LOCUS HUMGS000372 Human adult (K.Okubo) Homo sapiens cDNA 3', mRNA
DEFINITION sequence.

ACCESSION C21336.1 GI:1622446

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 18)

AUTHORS Okubo,K.

TITLE BodyMap: human gene expression database

JOURNAL Unpublished (1995)

COMMENT Contact: Okubo,K.

Institute for Molecular and Cellular Biol

Osaka University

1-3,Yamada-Oka, Suita, Osaka Pref. 565, Japan

Tel: 06-877-5111(ex.3315)

Email: kouzak@imcb.osaka-u.ac.jp

We are not submitting the same cDNA sequence redundantly to DBJ

since 1993. For the abundance information of clones with this

sequence in this library and as well as in other 3'-directed

libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The

sequences of the clones represented by this GS sequences is also

found there.

Location/Qualifiers

1..18

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="adult"

/clone_lib="Human adult (K.Okubo)"

/note="One or more human adult tissue"

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	13	Gaps:	0

US-09-966-880A-8 (1-198) x C21336 (1-18)

Qy 31 TyrValVal 33

Db 7 TATGTTGTG 15

RESULT 255

CA851280 18 bp mRNA linear EST 01-AUG-2003

LOCUS D12A08.B20.02.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max

DEFINITION cDNA clone D12A08 5', mRNA sequence.

ACCESSION CA851280

VERSION CA851280.1 GI:33388073

KEYWORDS EST.

SOURCE Glycine max (soybean)

ORGANISM Glycine max

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;

```

REFERENCE      1 (bases 1 to 18)
AUTHORS        Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE          Analysis of expressed sequence tags from roots of resistant soybean
                infected by the soybean cyst nematode
JOURNAL        Unpublished (2002)
COMMENT        Contact: Alkharouf, N.W.
                Soybean Genomics and Improvement Laboratory (SGIL)
                US Department of Agriculture (USDA), ARS, PSI
                Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
                USA
                Tel: 301 504 5750
                Fax: 301 504 5728
                Email: alkharouf@ars.usda.gov.
FEATURES       Location/Qualifiers
                source
                1..18
                /organism="Glycine max"
                /mol_type="cDNA"
                /cultivar="Peking"
                /db_xref="taxon:3847"
                /clone="D12A08"
                /tissue_type="Roots"
                /dev_stage="Seedlings"
                /clone_1ib="cDNA Peking library 2, 4 day SCN3"
                /note="Vector: pBluescript SK-, cDNA clones from mRNA
                extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Alignment Scores:
Pred. No.:      3 83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:          0
DB:             14          Gaps:            0

US-09-966-880A-8 (1-198) x CA851280 (1-18)

QY             172 LeuserArg 174
Db             12 CTNCTCGT 4

RESULT 256
LOCUS         CA851607              18 bp      mRNA      linear      EST 01-AUG-2003
DEFINITION   D15F01 K13.11.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
ACCESSION    CA851607
VERSION      CA851607.1 GI:333884400
KEYWORDS     EST.
SOURCE       Glycine max (soybean)
ORGANISM     Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 18)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..18
/organism="Glycine max"
/mol_type="mRNA"

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/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D15F01"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_1ib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-, cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Alignment Scores:
Pred. No.:      3 83e+06      Length:      18
Score:          3.00          Matches:      3
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:    1.52%        Indels:          0
DB:             14          Gaps:            0

US-09-966-880A-8 (1-198) x CA851607 (1-18)

QY             164 GlyLeuHis 166
Db             2 GGGCTACAT 10

RESULT 257
LOCUS         CD486685/c              18 bp      mRNA      linear      EST 01-JUL-2003
DEFINITION   CRHS.3A10 Cotton Root and Hypocotyl Lambda ZIPLOX library (CRH)
ACCESSION    CD486685
VERSION      CD486685.1 GI:31407650
KEYWORDS     EST.
SOURCE       Gossypium hirsutum (upland cotton)
ORGANISM     Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 18)
Dowd, C., Wilson, J. and McFadden, H.
Different Gene Expression Responses in Cotton Root and Hypocotyl
tissues during infection with Fusarium Wilt Disease
Unpublished (2003)
Contact: Caitriona Dowd, Helen McFadden
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Black Mountain Laboratories, Cnr Clunies Ross Street & Barry Drive,
Black Mountain, Canberra, ACT, 2601, Australia
Tel: 61 2 6246 4914, 6246 5377
Fax: 61 2 6246 5000
Email: Caitriona.Dowd@csiro.au, Helen.McFadden@csiro.au
Vector clipped sequences Bases 1-17 (GTGACCCACGCGTCCG): SalI
adapter
Seq primer: M13 reverse primer
High quality sequence stop: 18.
Location/Qualifiers
1..18
/organism="Gossypium hirsutum"
/mol_type="mRNA"
/cultivar="DeltaEMERALD"
/db_xref="taxon:3635"
/clone="CRHS.3A10"
/tissue_type="Root and hypocotyl tissues"
/dev_stage="5 day old seedlings"
/lab_host="Y1090(ZL)"
/clone_1ib="Cotton Root and Hypocotyl Lambda ZIPLOX
library (CRH)"
/note="Vector: Lambda ZIPLOX; Site 1: SalI; Site 2: NotI;
mRNA was prepared from root and hypocotyl tissues of the
cotton cultivar DeltaEMERALD. cDNA was synthesised from a
NotI-oligo(dT) primer/adaptor using the manufacturers
protocols (Life Technologies) and then ligated to a SalI
adaptor to facilitate directional cloning. The cDNA was
cloned into the SalI and NotI sites of the Lambda ZIPLOX

```

ORIGIN

phage vector (Life Technologies). Constructed by Catriona
Dowd and Helen McFadden."

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CD486685 (1-18)

Qy 106 LeuArgAsn 108

Db 15 TTGCGAATA 7

RESULT 258

CF308804

LOCUS 18 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--02-M04.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--02-M04, mRNA sequence.

ACCESSION CF308804

VERSION CF308804.1 GI:33680565

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gsbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. 18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--02-M04"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF308804 (1-18)

Qy 49 LeuArgAsn 51

Db 3 CTACGTAAC 11

RESULT 259

CF310639

LOCUS 18 bp mRNA linear EST 15-AUG-2003
DEFINITION ABF--05-G10.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-G10, mRNA sequence.

ACCESSION CF310639

VERSION CF310639.1 GI:33682400

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 18)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.
Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gsbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

source

1. 18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="ABF--05-G10"

/tissue_type="leaf"

/dev_stage="14 days after germination"

/lab_host="E.coli DH10B"

/clone_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive

element binding transcription factor 3 overexpression

line."

ORIGIN

Alignment Scores:

Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF310639 (1-18)

Qy 49 LeuArgAsn 51

Db 3 CTACGTAAC 11

RESULT 260

CF314452

LOCUS 18 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--02-P15.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--02-P15, mRNA sequence.

ACCESSION CF314452

VERSION CF314452.1 GI:33686213

KEYWORDS EST

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE
AUTHORS

Enthartoidae; Oryzae; Oryza.
1 (bases 1 to 18)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm, B.H.

Genomics and Genetics Institute, Greengene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

```
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--02-P15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF314452 (1-18)

Qy

49 leuAgaan 51

Db

3 CTACGTAAC 11

RESULT 261

CF317226/c

LOCUS

CF317226 18 bp mRNA linear EST 15-AUG-2003

DEFINITION

HD--06-N14.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

ACCESSION

CF317226

VERSION

CF317226.1 GI:33689897

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

AUTHORS

Enthartoidae; Oryzae; Oryza.

TITLE

1 (bases 1 to 18)

JOURNAL

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm, B.H.

JOURNAL

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

AUTHORS

of Bioscience and Bioinformatics, Myongji University

TITLE

Yongin, Kyeonggi, Korea

COMMENT

Tel: 82 31 330 6193

JOURNAL

Fax: 82 31 321 6355

FEATURES

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

source

Location/Qualifiers

1..18

ORIGIN

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-N14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
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Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF317226 (1-18)

Qy

58 GluLeuLeu 60

Db

12 GAGTGTGTG 4

RESULT 262

CF319738/c

LOCUS

CF319738 18 bp mRNA linear EST 15-AUG-2003

DEFINITION

HD--10-P16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA

ACCESSION

library (HD) Oryza sativa cDNA clone HD--10-P16, mRNA sequence.

VERSION

CF319738.1 GI:33691499

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

AUTHORS

Enthartoidae; Oryzae; Oryza.

TITLE

1 (bases 1 to 18)

JOURNAL

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

COMMENT

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm, B.H.

JOURNAL

Genomics and Genetics Institute, Greengene Biotech Inc.; Division

AUTHORS

of Bioscience and Bioinformatics, Myongji University

TITLE

Yongin, Kyeonggi, Korea

COMMENT

Tel: 82 31 330 6193

JOURNAL

Fax: 82 31 321 6355

FEATURES

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

source

Location/Qualifiers

```
1..18
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--10-P16"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
CDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
```

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF319738 (1-18)

Ory 85 SerProCys 87

Db 16 AGTCATGT 8

RESULT 263

CF323060

LOCUS HDN--02-N01.g1 OSHDACL-overexpressing transgenic rice lambda phage

DEFINITION CDNA library II (HDN) Oryza sativa CDNA clone HDN--02-N01, mRNA

ACCESSION

CF323060

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="HDN--02-N01"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 2 weeks"

/lab_host="E.coli SDR"

/clone_lib="OSHDACL-overexpressing transgenic rice lambda

phage CDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; CDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF323060 (1-18)

Ory 73 GlyArgCys 75

Db 7 GGCGGTGC 15

RESULT 264

CF330870/c

LOCUS NACL--06-M07.b1 Rice callus plasmid CDNA library (NACL) Oryza

DEFINITION sativa CDNA clone NACL--06-M07, mRNA sequence.

ACCESSION

CF330870

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--06-M07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid CDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF330870 (1-18)

Ory 85 SerProCys 87

Db 16 AGTCATGT 8

RESULT 265

CF332520

LOCUS JMT--01-A23.g1 AcJMT-overexpressing transgenic rice plasmid CDNA

library (JMT) Oryza sativa CDNA clone JMT--01-A23, mRNA sequence.

ACCESSION

CF332520

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 18

/organism="Oryza sativa"

/mol_type="mRNA"

/cultivar="Nackdong"

/db_xref="taxon:4530"

/clone="NACL--06-M07"

/tissue_type="callus"

/dev_stage="proliferated callus on 2N6 media for 30 days"

/lab_host="E.coli DH10B"

/clone_lib="Rice callus plasmid CDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

ORIGIN

Alignment Scores:

Pred. No.:	3.83e+06	Length:	18
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	14	Gaps:	0

US-09-966-880A-8 (1-198) x CF330870 (1-18)

Ory 85 SerProCys 87

Db 16 AGTCATGT 8

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source 1.18
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--01-A23"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF332520 (1-18)

OY 49 LeuArgAsn 51
|||||
Db 3 CTACGTAAAC 11

RESULT 266

CF333354 18 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--02-D13.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--02-D13, mRNA sequence.
ACCESSION CF333354
VERSION CF333354.1 GI:33814976
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source 1.18
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--02-D13"

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 14 Gaps: 0

US-09-966-880a-8 (1-198) x CF333354 (1-18)

OY 49 LeuArgAsn 51
|||||
Db 3 CTACGTAAAC 11

RESULT 267

CF334471 18 bp mRNA linear EST 18-AUG-2003
LOCUS JMT--03-M11.g1 AtUMT-overexpressing transgenic rice plasmid cDNA
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-M11, mRNA sequence.
ACCESSION CF334471
VERSION CF334471.1 GI:33817267
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 18)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc., Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source 1.18
Location/Qualifiers
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-M11"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtUMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="vector: PCR4-TOPO, Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

ORIGIN

Alignment Scores:
Pred. No.: 3.83e+06 Length: 18
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0
 DB: 14 Gaps: 0

US-09-966-880A-8 (1-198) x CF334471 (1-18)

QY 49 LeuArgAsn 51
 |||||
 3 CTACGTAC 11

RESULT 268
 D11637 18 bp mRNA linear EST 02-DEC-1992
 LOCUS HUM000C318 Liver HepG2 cell line. Homo sapiens cDNA clone c318,
 D11637 mRNA sequence.
 ACCESSION D11637.1 GI:2148229
 VERSION D11637
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 18)
 Okubo,K., Hori,N., Matoba,R., Niyama,T., Fukushima,A., Kojima,Y.
 and Matsubara,K.
 Large scale cDNA sequencing for analysis of quantitative and
 qualitative aspects of gene expression
 Nat. Genet. 2, 173-179 (1992)

JOURNAL MEDLINE 94258199
 PUBMED 1345164
 CONTACT: Kousaku Okubo, Naohiro Hori, Ryo Matoba, Toshiyuki
 Niyama, Atsushi Fukushima, Yoko Kojima & Kenichi Matsubara
 Institute for Molecular and Cellular Biology
 Osaka University
 1-3 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
 source
 1. 18
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:DS7522E"
 /db_xref="taxon:9606"
 /clone="c318"
 /lab_host="E.coli"
 /clone_1b="Liver HepG2 cell line."
 /note="3'-directed regional cDNA library. Cleaved by MboI
 and transformed into E.coli."

ORIGIN
 Alignment Scores:
 Pred. No.: 3.83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x D11637 (1-18)

QY 31 TyrValVal 33
 |||||
 7 TATGTTGTG 15

RESULT 269
 L76122 18 bp mRNA linear EST 21-FEB-1996
 LOCUS SCMRAP0216 G2/KS adult worm mini-library Schistosoma mansoni cDNA
 DEFINITION clone SCMRAP0216, mRNA sequence.
 L76122
 ACCESSION L76122.1 GI:1196860
 VERSION L76122
 KEYWORDS EST.
 SOURCE Schistosoma mansoni
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidae; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 18)
 AUTHORS Neto,E.D., Harrop,R, Correa-Oliveira,R, Wilson,R.A., Pena,S.D. and
 Simpson,A.U.G.
 TITLE Mini-libraries constructed from cDNA generated by arbitrarily primed
 RT-PCR: an alternative to normalized libraries for the generation
 of ESTs from nanogram quantities of mRNA
 JOURNAL Gene 186 (1), 135-142 (1997)
 MEDLINE 97199380
 PUBMED 9047356
 COMMENT Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A.,
 Pena,S.D. and Simpson,A.U.G.
 Location/Qualifiers
 1. 18
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SCMRAP0216"
 /note="A mini-library was made by cloning products derived
 from RNA-arbitrarily primed PCR (RAP PCR) profiles into
 the pUC 18 vector. Reverse transcription of adult worm
 mRNA was primed with G2 and subsequent PCR amplification
 was performed in the presence of primer KS"

ORIGIN
 Alignment Scores:
 Pred. No.: 3.83e+06 Length: 18
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 Gaps: 0

US-09-966-880A-8 (1-198) x L76122 (1-18)

QY 185 GluValAsp 187
 |||||
 11 GAGGTGCAC 3

RESULT 270
 HSM007596 standard; mRNA; EST; 19 BP.
 ID HSM007596
 AC AL042746;
 SV AL042746.1

DT 12-MAR-1999 (Rel. 59, Created)
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)

DE Homo sapiens mRNA; EST DKFZp434C1822_r1 (from clone DKFZp434C1822)
 KW EST; expressed sequence tag.

OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.

CC [1]
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
 Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
 RL MIPS, Am Klopferpitz 18a D-82152 Martinsried, GERMANY
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA
 CC sequencing consortium of the German Genome Project
 CC No st sequence available
 CC This clone is available at the RZPD in Berlin
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers

```

FH source 1..19
FT /db_xref="taxon:9606"
FT /mol_type="mRNA"
FT /organism="Homo sapiens"
FT /clone_lib="434 (synonym: hres3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;

Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x HSM007596 (1-19)

QY 131 ArgAlaGly 133
DB 1 CGCGCGCGGT 9

RESULT 271
HSM007596/c
ID HSM007596 standard; mRNA; EST; 19 BP.
XX AL042746;
XX SV AL042746.1
XX DT 12-MAR-1999 (rel. 59, Created)
XX DT 12-MAR-1999 (rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434C1822_r1 (from clone DKFZp434C1822)
XX EST; expressed sequence tag.
XX OS Homo sapiens (human)
XX OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX RN [1]
XX RP 1-19
XX RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX RL MIPS, Am Kiofererspitze 18a D-82152 Martinsried, GERMANY
XX CC Clone from S. Wiemann, sequenced by LMU within the CDNA
XX CC sequencing consortium of the German Genome Project
XX CC No si sequence available
XX CC This clone is available at the RZPD in Berlin
XX CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
XX CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
FH Key Location/Qualifiers
FH 1..19
FH source /db_xref="taxon:9606"
FH /mol_type="mRNA"
FH /organism="Homo sapiens"
FH /clone_lib="434 (synonym: hres3). Vector pSport1; host
FH DH10B; sites NotI + SalI"
FH /dev_stage="adult"
FH /tissue_type="testis"
SQ Sequence 19 BP; 2 A; 8 C; 6 G; 3 T; 0 other;

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```

Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880A-8 (1-198) x HSM007596 (1-19)

QY 193 PheArgThr 195
DB 15 TTCGGAGCC 7

RESULT 272
AA884867/c
LOCUS AA884867/c
DEFINITION aa884867 19 bp mRNA linear EST 04-JUN-1999
am21d11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1467453 3' similar to TR:Q93040 Q93040 TIF1BETA ZINC FINGER
PROTEIN. [1] ; mRNA sequence.
ACCESSION AA884867.1 GI:2994848
VERSION AA884867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CCAG http://www.ncbi.nlm.nih.gov/ncicagap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAG Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 1216 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source
1..19
Location/Qualifiers
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1467453"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pT773D-Pec (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH119, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and as circles were made in
vitro. Following RNP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bernaldo."
ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

```

US-09-966-880A-8 (1-198) x AA884867 (1-19)

QY 172 LeuSerArg 174

DB 11 CTGTACGCA 3

RESULT 273
AA903030

LOCUS AA903030 19 bp mRNA linear EST 19-MAY-1998
DEFINITION Ok51a08.s1 NCI CGAP Le12 Homo sapiens cDNA clone IMAGE:1517462 3'

ACCESSION AA903030 similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ; mRNA sequence.

VERSION AA903030.1 GI:3038153

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL 1 (bases 1 to 19)

COMMENT Contact: Robert Strausberg, Ph.D.

Unpublished (1997)

Email: cgapsb@mail.nih.gov

unknown library type

Trace considered overall poor quality

Insert Length: 714 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1.19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1517462"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B"

/clone_lib="NCI CGAP Le12"

/note="Organ: soft tissue; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Site 1: Not I; Site 2: Eco RI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

15'-AACTGGAAGATTCGCGCGCAATCTTTTCTTTTCTTTT-3';

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

ALIGNMENT SCORES:

Pred. No.: 4.05e+06 Length: 19

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA903030 (1-19)

QY 145 PheTyCys 147

DB 2 TTTATTGT 10

RESULT 274

AA918795

LOCUS

DEFINITION

AA918795

VERSION

KEYWORDS

AA918795

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL 1 (bases 1 to 19)

COMMENT Contact: Robert Strausberg, Ph.D.

Unpublished (1997)

Email: cgapsb@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/ILN at:

www.bio.lim.gov/bdrp/image/image.html

Trace considered overall poor quality

Insert Length: 814 Std Error: 0.00

Seq primer: -40m3 fwd. ET from Amerham

High quality sequence stop: 1.

Location/Qualifiers

1.19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1534856"

/tissue_type="DH10B"

/lab_host="DH10B"

/clone_lib="NCI CGAP Kid3"

/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer,

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified pT73 vector. mRNA

source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and

M. Fatima Bonaldo."

ALIGNMENT SCORES:

Pred. No.: 4.05e+06 Length: 19

Score: 3.00 Matches: 3

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 1.52% Indels: 0

DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x AA918795 (1-19)

QY 23 GlyArgArg 25

DB 11 GGGAGGAGG 19

RESULT 275

AA918795/c

LOCUS AA918795/c

DEFINITION AA918795 19 bp mRNA linear EST 10-JUN-1998

0169c05.s1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1534856 3'

similar to TR:Q39595 Q39595 EXTENSIN ; contains TAR1.b2 TAR1

repetitive element ; mRNA sequence.

ACCESSION AA918795

VERSION AA918795.1 GI:3058685

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL
COMMENT

Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

FEATURES

Source

Trace considered overall poor quality
 Insert Length: 814 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

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1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1534856"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_Kid3"
/note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x AA918795 (1-19)

QY 180 LeuLeuPro 182
 |||||
 |||||
 DB 18 CTCCTCCCC 10

RESULT 276

AA932041

LOCUS AA932041 19 bp mRNA linear EST 07-JUN-1998
 DEFINITION c035h05.s1 NCI CGAP LUS Homo sapiens cDNA clone IMAGE:1568217 3', similar to SW:NTM PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4', mRNA sequence.

ACCESSION AA932041 GI:3087083
 VERSION AA932041.1 GI:3087083
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.

JOURNAL
COMMENT

FEATURES

Source

cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 525 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

```
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1568217"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI-CGAP_LUS"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
```

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: Gaps: 0

US-09-966-880A-8 (1-198) x AA932041 (1-19)

QY 103 AsnLeuSer 105
 |||||
 |||||
 DB 10 AATTGAGT 18

RESULT 277

AA934303/c

LOCUS AA934303/c 19 bp mRNA linear EST 26-MAR-1999
 DEFINITION SWOV13CAN12H12 Onchocerca volvulus infective larva cDNA (SAM94WV-OVL3) Onchocerca volvulus cDNA clone onch672 5' similar to TR:Q33571 Q33571 ATP5B SUBUNIT 6', mRNA sequence.

ACCESSION AA934303
 VERSION AA934303.1 GI:3091460
 KEYWORDS EST.
 SOURCE Onchocerca volvulus
 ORGANISM Onchocerca volvulus

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.
 1 (bases 1 to 19)
 Williams, S.A., Lizotte-Waniewski, M., Laney, S., Wenhong, L., Hillier, L., Allen, M., Bowles, L., Gelsel, S., Joet, S., Kucaba, T., Martin, J., Steptoe, M., Theising, B., White, Y., Wylie, T., Chappell, J., Person, B., Gibbons, M., Harvey, N., Pape, D., Chamberlain, A., Morales, R., Schurk, R., Riteer, B., Kohn, S., Underwood, K. and Marra, M.
 Molecular Parasitology OVL3
 Unpublished (1998)
 Contact: Steven A. Williams
 Molecular Parasitology
 Smith College Department of Biological Sciences
 Department of Biological Sciences, Clark Science Center, Smith College, Northampton, MA, 01063, USA
 Tel: 4135853826
 Fax: 4135853786
 Email: genome@smith.edu

JOURNAL
COMMENT

The library was constructed by Menhong Lu. The library is available from Dr. S.A. Williams, email genomesmith.edu When requesting this clone from Dr. Williams, please reference the Williams lab clone id - SMOV33CAN12H12
 Seq primer: -40m13 fwd. RT from Amerham
 High quality sequence stop: 1.

FEATURES

source

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1. 19
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/strain="Sierra Leone"
/db_xref="taxon:6282"
/clone="onch672"
/lab_host="XLI-Blue MRF"
/clone_lib="Onchocerca volvulus infective larva cDNA (SAM94UL-OvL3)"
/note="Vector: lambda UniZap XR; Site 1: EcoR I; Site 2: Xho I; Cutaneous filarial nematode parasite of humans. mRNA was prepared from third stage infective larvae of Onchocerca volvulus isolated from mosquitoes 10 days after infection and converted to double stranded cDNA using reverse transcriptase and oligo(dT) followed by Kase H and DNAPol I. The library had 1.8 x 10E5 independent recombinants and average insert size was 900 base pairs. The library was constructed by Menhong Lu. The library is available from Dr. S.A. Williams, email genomesmith.edu."
```

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AA934303 (1-19)

CY 60 Leuphelen 62

DB 17 CTTTITTTG 9

RESULT 278

AI016864/C

LOCUS

DEFINITION

AI016864 19 bp mRNA linear EST 27-AUG-1998
 ou27c11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:1627508 3' similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE
 SUBUNIT 1 ; mRNA sequence.

AI016864.1 GI:3231200

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 This clone is available royalty-free through LMLT ; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Trace considered overall poor quality
 Insert length: 358 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amerham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

```
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

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/clone="IMAGE:1627508"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  

a modified polylinker; Site 1: Not I; Site 2: Eco RI;  

Equal amounts of plasmid DNA from three normalized  

libraries (fetal lung NbH19W, testis NHT, and B-cell  

NCI CGAP GCBI) were mixed, and ss circles were made in  

vitro. Following HAP purification, this DNA was used as  

tracer in a subtractive hybridization reaction. The driver  

was PCR-amplified cDNAs from pools of 5,000 clones made  

from the same 3 libraries. The pools consisted of  

I.M.A.G.E. clones 297480-302087, 682632-687239,  

726408-728711, and 729096-731399. Subtraction by Bento  

Soares and M. Fatima Bonaldo."
```

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x AI016864 (1-19)

CY 83 SerTpsr 85

DB 15 TCCTGCTCT 7

RESULT 279

AI017940

LOCUS

DEFINITION

AI017940 19 bp mRNA linear EST 27-AUG-1998
 ou24b04.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
 IMAGE:1627183 3' similar to SW:ME4C DROME Q01644 MALE SPECIFIC
 SPERM PROTEIN MST84DC ; contains TAA1.t3 TAA1 repetitive element ;
 mRNA sequence.

AI017940.1 GI:3232276

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

source

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 This clone is available royalty-free through LMLT ; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Trace considered overall poor quality
 Insert length: 1853 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amerham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

```
1. 19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1627183"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pTZ19-Pac (Pharmacia) with  

a modified polylinker; Site 1: Not I; Site 2: Eco RI;  

Equal amounts of plasmid DNA from three normalized  

libraries (fetal lung NbH19W, testis NHT, and B-cell  

NCI CGAP GCBI) were mixed, and ss circles were made in  

vitro. Following HAP purification, this DNA was used as  

tracer in a subtractive hybridization reaction. The driver
```

was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1 M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

Best Local Similarity: 100.00%
Query Match: 1.52%
DB: 9
Gaps: 0

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A107581 (1-19)

QY 118 AsparGly 120
DB 1 GACCGCAA 9

RESULT 280

A1077581 19 bp mRNA linear EST 24-SEP-1998
LOCUS A1077581
DEFINITION oy26a04.s1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA
clone IMAGE:166526 3' similar to SW:P31 HUMAN P48556 26S
PROTEASOME REGULATORY SUBUNIT P31. ; mRNA sequence.

ACCESSION A1077581
VERSION A1077581.1 GI:3411989
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
This clone is available royally-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 897 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:166526"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts NbHSF"
/note="Vector: pRTT3D (Pharmacia) with a modified
polylinker V-type; phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0

US-09-966-880A-8 (1-198) x A107581 (1-19)
QY 104 LeuSerLeu 106
DB 6 TTAAGCTC 14

Best Local Similarity: 100.00%
Query Match: 1.52%
DB: 9
Gaps: 0

US-09-966-880A-8 (1-198) x A107581 (1-19)

QY 195 ThrLeuGly 197
DB 4 ACACTGGCT 12

RESULT 281

A1078728 19 bp mRNA linear EST 24-SEP-1998
LOCUS A1078728
DEFINITION oy12i07.s1 Soares senescent fibroblasts NbHSF Homo sapiens CDNA
clone IMAGE:166537 3' similar to SW:POR2 HUMAN P45880
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2 ; mRNA
sequence.

ACCESSION A1078728
VERSION A1078728.1 GI:3411650
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
This clone is available royally-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 575 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
source Location/Qualifiers
1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:166537"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares senescent fibroblasts NbHSF"
/note="Vector: pRTT3D (Pharmacia) with a modified
polylinker V-type; phagemid; Site 1: Not I; Site 2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3',
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRTT3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M. Fatima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

ORIGIN

US-09-966-880A-8 (1-198) x A1078728 (1-19)
QY 104 LeuSerLeu 106
DB 6 TTAAGCTC 14

RESULT 282
A1147066/c
LOCUS A1147066 19 bp mRNA linear EST 29-SEP-1998
DEFINITION OX33b08.s1 Soares NSF P8 9W OT PA.P S1 Homo sapiens cDNA clone IMAGE:1509591.3' similar to TR:O05039 009039 LINKER OF T-CELL RECEPTOR PATHWAYS ; contains TARI.t2 TARI repetitive element ;, mRNA sequence.

ACCESSION A1147066
VERSION A1147066.1 GI:3674748
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 19)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES
Source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1509591"
/lab_host="DH10B"
/clone_lib="Soares NSF P8 9W OT PA.P S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NBHSF pool 1: 309384-310919, 323208-325895 Soares NB2HP pool 1: 145032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares NB2HP-9W pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 304776-306311, 320136-322823, 326280-326663 Soares NBHOT pool 1: 723720-726407, 739080-740999. Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880a-8 (1-198) x A1147066 (1-19)

QY 171 ArgLeuser 173
Db 12 AGCTTCA 4

RESULT 283
A1155325
LOCUS A1155325 19 bp mRNA linear EST 30-SEP-1998
DEFINITION ud88a05.r1 Soares NMPu Mus musculus cDNA clone IMAGE:1477904.5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;, mRNA sequence.

ACCESSION A1155325

VERSION A1155325.1 GI:3683794
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 19)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The Washu-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.
WGI:926260
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 RT from Amersham
High quality sequence stop: 1.

FEATURES
Source
1..19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1477904"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Soares NMPu"
/note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: Gaps: 0

US-09-966-880a-8 (1-198) x A1155325 (1-19)

QY 172 LeuserArg 174
Db 4 CTATCTCA 12

RESULT 284
A1360784/c
LOCUS A1360784 19 bp mRNA linear EST 15-FEB-1999
DEFINITION G958g07.r1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2010588.3' similar to TR:Q41707 Q41707 EXTENSIN CLASS 1 PROTEIN PRECURSOR. ;, mRNA sequence.

ACCESSION A1360784
VERSION A1360784.1 GI:4112405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 653 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1.19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2120736"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP Lym12"
 /note="Organ: lymph node; Vector: PCMV-SPORT6; Site 1:
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1431460 (1-19)

QY 130 Hsargala 132

Db 3 CACAGGCC 11

RESULT 287

A1433480

LOCUS

DEFINITION

A1433480 19 bp mRNA linear EST 30-MAR-1999
 t153a06.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134162 3'
 similar to SW:BRPc HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
 ; contains element TART repetitive element ; mRNA sequence.

ACCESSION A1433480

VERSION A1433480.1 GI:4289474

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Life Technologies catalog #: 11547-015
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1003 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1.19
 /organism="Homo sapiens"

/mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2134162"
 /tissue_type="lymphoma, follicular mixed small and large
 cell"
 /lab_host="DH10B"
 /clone_lib="NCI-CGAP Lym12"
 /note="Organ: lymph node; Vector: PCMV-SPORT6; Site 1:
 SalI; Site 2: NotI; Cloned unidirectionally. Primer:
 Oligo dt. Average insert size 1.25 kb. Life Technologies
 catalog #: 11547-015"

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1433480 (1-19)

QY 72 Proglyarg 74

Db 10 CCGGCGCG 18

RESULT 288

A1524591/c

LOCUS

DEFINITION

A1524591 19 bp mRNA linear EST 12-MAY-1999
 t043f09.x1 NCI CGAP U4 Homo sapiens cDNA clone IMAGE:2181833 3'
 similar to SW:NU4M PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE
 CHAIN 4 ; mRNA sequence.

ACCESSION A1524591

VERSION A1524591.1 GI:4438726

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
 www.bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 502 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1
 POLVA-No.

FEATURES

source

1.19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2181833"
 /tissue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP U4"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

US-09-966-880A-8 (1-198) x A1583857 (1-19)

QY 139 MetThrphe 141

DB 11 ATGACGTC 3

RESULT 291

A1584018 19 bp mRNA linear EST 14-DEC-1999

LOCUS t312e10.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:228394 3' similar to SW:FRPL_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO ;, RNA sequence.

ACCESSION A1584018 GI:4569915

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbtp/image/image.html

Trace considered overall poor quality
Insert Length: 396 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA-No.

FEATURES Location/Qualifiers

1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:228394"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT6, Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1584018 (1-19)

QY 72 ProglyArg 74

DB 8 CCGGCCGC 16

RESULT 292

A1597783 19 bp mRNA linear EST 14-MAY-1999

LOCUS t122g04.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2226582 3' similar to SW:DX3_MOUSE Q62167 DEAD BOX PROTEIN 3 ;, mRNA sequence.

ACCESSION A1597783

VERSION A1597783.1 GI:4606831

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 19) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbtp/image/image.html
Insert Length: 842 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA-No.

FEATURES Location/Qualifiers

1..19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2226582"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Panl"
/note="Organ: pancreas; Vector: pCMV-SPORT6, Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
Score: 3.00 Matches: 3
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.52% Indels: 0
DB: 9 Gaps: 0

US-09-966-880A-8 (1-198) x A1597783 (1-19)

QY 39 AlaThrSer 41

DB 11 GCCACCTCC 19

RESULT 293

A1664013 19 bp mRNA linear EST 10-MAY-1999

LOCUS ue7a1.r1 Scores NMPu Mus musculus cDNA clone IMAGE:1496732 5' similar to TR:O89050 O89050 MUSKELIN. ;, mRNA sequence.

ACCESSION A1664013 GI:4767596

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 19) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:934336

Trace considered overall poor quality
 Possibly reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..19
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:1496732"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

/clone_lib="Soares_NMPu"
 /note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1664013 (1-19)

QY 35 ArgArgasp 37

Db 1 AGAAGAGAC 9

RESULT 294

A1664013/c

LOCUS

A1664013 19 bp mRNA linear EST 10-MAY-1999

DEFINITION

ue73a11.r1 Soares NMPu Mus musculus cDNA clone IMAGE:1496732 5', similar to TR:089050 089050 MUSKELIN. ;, mRNA sequence.

ACCESSION

A1664013

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1496732"

/sex="female"

/dev_stage="adult"

/lab_host="DH10B"

/lab_host="DH10B"

/lab_host="DH10B"

/lab_host="DH10B"

/lab_host="DH10B"

/clone_lib="Soares_NMPu"
 /note="Organ: uterus; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pregnant mouse uterus, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1664013 (1-19)

QY 104 LeuSerLeu 106

Db 11 TTGTCTCTT 3

RESULT 295

A1747751/c

LOCUS

A1747751 19 bp mRNA linear EST 22-JUN-1999

DEFINITION

u121h05.x1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2088249 3' similar to TR:P79101 CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN. ;, mRNA sequence.

ACCESSION

A1747751

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..19

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:2088249"

/dev_stage="embryo, 14 dpc"

/lab_host="DH10B"

/clone_lib="Sugano mouse embryo mewa"

/note="Vector: pWE18-FL3; Site 1: DraIII (CACTGCTG); Site 2: DraIII (CACTGCTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

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double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

double-stranded cDNA was ligated to a DraIII adaptor

ORIGIN

[TGTGTGGCTACTG], digested and cloned into distinct DraIII sites of the pME18S-PL3 vector (5' site CACGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAGAGCTGG and 3' end primer CGACCTGCAGCTCGAGCACA."

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1747751 (1-19)

QY 104 LeuSerLeu 106
 DB 11 CTCTCCTG 3

RESULT 296
 A1758301 19 bp mRNA linear EST 16-DEC-1999
 LOCUS A1758301/c ty06a07.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278260 3'
 DEFINITION similar to SW:SP49 HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49
 ;contains MSRI.b2 MSRI repetitive element //, mRNA sequence.

ACCESSION A1758301.1 GI:5152024
 VERSION EST
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE

JOURNAL Unpublished (1997)
 COMMENT

CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLMT at:
 www-bio.llnl.gov/bbrp/image/image.html

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1803 Std Error: 0.00
 Seq primer: -40UP from Gibco

High quality sequence stop: 1.
 Location/Qualifiers

1. .19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2278260"
 /tissue_type="poorly-differentiated endometrial
 adenocarcinoma, 2 pooled tumors"
 /lab_host="MDH10B"
 /clone_lib="NCI CGAP Ut3"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.45 kb. Life Technologies catalog #:
 11541-018"

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1758301 (1-19)

QY 23 GIATGATG 25
 DB 13 GCGAGCGCG 5

RESULT 297
 A1811474 19 bp mRNA linear EST 15-DEC-1999
 LOCUS A1811474 tw43c04.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2262438 3'
 DEFINITION similar to TR:O61645 O61649 PYROLIDONE-RICH ANTIGEN. ;contains
 element MSRI repetitive element //, mRNA sequence.

ACCESSION A1811474.1 GI:5398040
 VERSION EST
 KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM

REFERENCE Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 19)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 TITLE

JOURNAL Unpublished (1997)
 COMMENT

CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLMT at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Insert Length: 1729 Std Error: 0.00
 Seq primer: -40UP from Gibco

High quality sequence stop: 1.
 Location/Qualifiers

1. .19
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2262438"
 /tissue_type="well-differentiated endometrial
 adenocarcinoma, 7 pooled tumors"
 /lab_host="MDH10B"
 /clone_lib="NCI CGAP Ut1"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Life Technologies catalog #:
 11538-014"

FEATURES

source

1. .19

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2262438"

/tissue_type="well-differentiated endometrial
 adenocarcinoma, 7 pooled tumors"
 /lab_host="MDH10B"
 /clone_lib="NCI CGAP Ut1"
 /note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.75 kb. Life Technologies catalog #:
 11538-014"

FEATURES

source

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880A-8 (1-198) x A1811474 (1-19)

CY 23 GATGATG 25
 DB 5 GAGAGGCGG 13
 RESULT 298
 LOCUS A1918188 19 bp mRNA linear EST 13-DEC-1999
 DEFINITION tnn8c09.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2167024 3'
 ACCESSION A1918188
 VERSION A1918188
 KEYWORDS A1918188.1 GI:5638043
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS NCI/NIHNS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index
 COMMENT Unpublished (1998)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgaps-rc@mail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILMN at:
 www.bio.illn.gov/bdrp/image/image.html
 Insert Length: 1154 Std Error: 0.00
 Seq primer: -40UP from G1bco
 High quality sequence stop: 1.
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2167024"
 /tissue_type="anaplastic oligodendroglioma"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Brn25"
 /note="Organ: Brain; Vector: pTT3D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTCACATCTGAGTGGAGCGCGCATGATGTTTTTTTTTTTTTTT
 T 3']: double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pTT3D vector.
 Library is normalized, and was constructed by Bento
 Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A1918188 (1-19)

CY 30 CysTyrVal 32
 DB 16 TGTATGATG 8
 RESULT 299
 A0061154

LOCUS A0061154 19 bp mRNA linear EST 20-MAY-1999
 DEFINITION A0061154 Dictyostelium discoideum SL (H.Urushihara) Dictyostelium
 discoideum cDNA clone SLD408, mRNA sequence.
 ACCESSION A0061154
 VERSION A0061154.1 GI:4882258
 KEYWORDS EST.
 SOURCE Dictyostelium discoideum
 ORGANISM Dictyostelium discoideum
 Eukaryota; Mycetozoa; Dictyostelidae; Dictyostelium.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Morio,T., Urushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M.,
 Yoshino,R., Mitsu,B.N., Pi,M., Saito,T., Takemoto,K., Yasukawa,H.,
 Williams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.
 TITLE Developmental cDNA in Dictyostelium discoideum
 JOURNAL Unpublished (1998)
 COMMENT Contact: Hideko Urushihara
 Institute of Biological Sciences
 University of Tsukuba
 1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
 Tel: 81-298-53-4664
 Fax: 81-298-53-6614
 Email: hidekobiol.tsukuba.ac.jp
 PROJECT = Dictyostelium discoideum cDNA project in Japan.
 Location/Qualifiers
 1..19
 /organism="Dictyostelium discoideum"
 /mol_type="mRNA"
 /strain="AX4"
 /db_xref="taxon:44689"
 /clone="SLD408"
 /dev_stage="slug"
 /clone_lib="Dictyostelium discoideum SL (H.Urushihara)"

ORIGIN

Alignment Scores:
 Pred. No.: 4.05e+06 Length: 19
 Score: 3.00 Matches: 3
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.52% Indels: 0
 DB: 9 Gaps: 0

US-09-966-880a-8 (1-198) x A0061154 (1-19)

CY 74 ArgCysTyr 76
 DB 4 AGATGTTAT 12

RESULT 300

LOCUS AM059909 19 bp mRNA linear EST 23-AUG-2000
 DEFINITION AHutr best upc15.ba.A040ell upc15 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AM059909
 VERSION AM059909.1 GI:6652231
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 19)
 Brenner,S., Williams,S.R., Vertmass,B.H., Storck,T., Moon,K.,
 McCoilum,C., Mao,J.I., Kirchner,D.J., Ellett,S., Dubridge,R.B.,
 Burcham,T. and Albrecht,G.
 In vitro cloning of complex mixtures of DNA on microbeads: Physical
 separation of differentially expressed cDNAs
 Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

TITLE

JOURNAL MEDLINE
 PUBMED
 CONTACT: Burcham TS
 LYNX Therapeutics, Inc.
 25861 Industrial Blvd., Hayward, CA 94545, USA
 Tel: 510 670 9338
 Fax: 510 670 9302

Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megascort technology.
Collected from the up-regulated gate.
High quality sequence stop: 19.
Location/Qualifiers
1. 19
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_id="UPC15"
/note="Vector: pCR2.1; Cloning of PCR products from
micro-beads carrying 3' end of up-regulated cDNA. THP-1
cells induced with 100 nM PMA in DMSO."

ORIGIN

Alignment Scores:

Pred. No.:	4.05e+06	Length:	19
Score:	3.00	Matches:	3
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.52%	Indels:	0
DB:	9	Gaps:	0

US-09-966-880a-8 (1-198) x AM059909 (1-19)

QY 195 ThrLeuGly 197
|||
Db 3 ACTTGCGA 11

Search completed: March 5, 2004, 02:19:27
Job time : 2522 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 20:57:37 ; Search time 360 Seconds
(without alignments)
7044.928 Million cell updates/sec

Title: US-09-966-880a-7_COPY_80_676

Sequence: 1 atggagacagcccttgatgaa.....ttcgtacttggagacttga 597

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1690386

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database : N_Geneseq_299a04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	2.5	17	2	AAA20708 Integrin
2	15	2.5	20	3	AAZ75674 Human b1a
3	14	2.3	16	3	AA13058 Antisense
4	14	2.3	17	2	AAA20709 Integrin
5	14	2.3	17	9	ABT34570 Tumour su
6	14	2.3	17	9	ADB42497 Tumour su
7	14	2.3	20	2	AAV09174 Phospho
8	14	2.3	20	2	AAV09175 Phospho
9	14	2.3	20	6	ABZ30588 Candida a
10	14	2.3	20	7	ACA90226 Novel hum
11	14	2.3	20	9	ADC26512 NOV prote
12	13	2.2	17	6	ABT05327 Human N-a
13	13	2.2	17	6	ABK24744 Glyphos
14	13	2.2	17	6	ABK24743 Glyphos
15	13	2.2	17	6	ABV79549 Human HTP
16	13	2.2	17	6	ABV79553 Human HTP
17	13	2.2	17	6	ABV79551 Human HTP
18	13	2.2	17	6	ABV79552 Human HTP
19	13	2.2	17	6	ABV79550 Human HTP
20	13	2.2	17	6	ABJ31517 Human HLA
21	13	2.2	17	7	ACC53477 Human tum
22	13	2.2	17	7	ADA99326 Human MDZ
23	13	2.2	17	7	ADA99325 Human MDZ

C 24	13	2.2	17	7	ADA99327
C 25	13	2.2	17	7	ADA99324
C 26	13	2.2	17	7	ADA99328
C 27	13	2.2	17	7	ABZ61946 Human H-R
C 28	13	2.2	17	7	ABZ61384 Human H-R
C 29	13	2.2	18	3	AAZ44774 Human FAD
C 30	13	2.2	19	2	AAZ41855 Probe/prl
C 31	13	2.2	19	3	AAA83045 cdk6 ribo
C 32	13	2.2	19	3	AAA83046 cdk6 ribo
C 33	13	2.2	19	4	AAI65672 Primer fo
C 34	13	2.2	19	5	AAH58207 Cell-cycl
C 35	13	2.2	19	5	AAH58208 Cell-cycl
C 36	13	2.2	19	7	ACP03639 Human NOV
C 37	13	2.2	20	2	AAQ71065 Primer #1
C 38	13	2.2	20	2	AAV68469 Oligo con
C 39	13	2.2	20	2	AAZ37511 Human mdm
C 40	13	2.2	20	2	AAZ37511 Human mdm
C 41	13	2.2	20	3	AAZ87306 PRO509 re
C 42	13	2.2	20	3	AAA38137 Polynucle
C 43	13	2.2	20	3	AAAC0546 Human fra
C 44	13	2.2	20	4	AAZ46974 Probe use
C 45	13	2.2	20	5	AAZ80665 Human mdm
					AAZ29280 Human mdm

ALIGNMENTS

RESULT 1
ID AAA20708 standard; RNA, 17 BP.
AC AAA20708;
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3934.
XX
XX Human, aryl hydlocarbon nuclear transport; ARNT, TIE-2; angiogenesis;
KW Integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytoskeletal; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipeptidic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW amyotic degeneration; psoriasis; verruca vulgaris; angiodiroma;
KW tuberculous sclerosis; pot-wine strain; Sturge Weber syndrome;
KW Kippel-Trenunay-Weber syndrome; Oeler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
OS
XX
XX MO9950403-AZ.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99MO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
PI WPI, 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
PT of an mRNA encoding an angiogenic factor.
XX
XX Claim 55; Page 162; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AA1675 to
CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,

CC and AAA17166 to AAA17560 and AAA17623 to AAA17684 represent their CC corresponding target sequences; AAA17685 to AAA19385 and AAA19087 to AAA19154 represent ribozyme sequences for Tle-2, and AAA1836 to AAA19086 and AAA19155 to AAA19222 represent their corresponding target sequences; AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and AAA21596 to AAA21688 represent their corresponding target sequences; AAA21689 to AAA22475 and AAA22363 to AAA22342 represent ribozyme sequence for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to AAA23422 represent their corresponding target sequences. The ribozymes of the invention are used for modulating the synthesis, expression and/or stability of an mRNA encoding angiogenic factor, especially ANNT.

CC integrin subunit beta-3, integrin subunit alpha-6, or Tle-2. They are especially used to treat cancer, diabetic retinopathy, age related macular degeneration (ARMD), inflammation, and arthritis, as well as neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris, angiolipoma of tuberosus sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome, CC and other syndromes and diseases related to the levels of ANNT, Tle-2, CC integrin subunit alpha-6, or integrin subunit beta-3

XX Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

Query Match	2.5%	Score 15;	DB 2;	length 17;
Best Local Similarity	73.3%	Pred. No. 3.7e+03;		
Matches 11; Conservative	4;	Mismatches 0;	Indels 0;	Gaps 0

```
QY      36 TTACCAATTCAAAA 50
          ::|||::|||
Db      1  UUACCAUUCAAAA 15
```

RESULT 2
AAZ75674/c
ID AAZ75674 standard; DNA; 20 BP.

AC	AAZ75674;
XX	
DT	10-SEP-2001 (first entry)
..	

Human biallelic marker downstream amplification primer SEQ ID NO:10030.

KM Human genome; biallelic marker; high density disequilibrium map
 KM genomic map; haplotype; phenotype; polymorphic base; genotyping
 KM haployping; hybridisation; identification; characterisation;
 KM amplification; single nucleotide polymorphism; SNP; PCR primer;
 KM amplicons; ss.

OS Homo sapiens.

PN WO9954500-A2.

PD 28-OCT-1999.

PF 21-APR-1999; 99MO-IB000822.

PR 21-APR-1998; 98US-0082614P.

XXXXXX

2000

2000

2 3

PT map of the human genome.

PS Claim 8; Page 2369; 2745pp; English.

CC AA265554 to AA265578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA265579 to AA277440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
CC
CC
CC
CC Sequence 20 BP, 6 A, 5 C, 3 G, 6 T, 0 U, 0 Other;
CC
CC
CC
CC

Query Match	2.5%;	Score 15;	DB 3;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 3.7e+03;		
Matches	15;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

Qy	24	GAGGAAGTTCTTTA	38
Db	15	GAGGAAGTTCTTTA	1

RESULT 3
AAA13058/c
ID AAA13058 standard; DNA; 16 BP.

AC	AAA13058;
XX	
DT	14-JUL-2000 (first entry)

DE Antisense oligonucleotide #16 targeting the PTS operon

KW Antisense oligonucleotide; treat; inhibit translation; diagnose;

KW nutrient uptake; bacterial infection; PTS operon; *Haemophilus influenzae*;

[illegible]

<p> </p>	<p> </p>
--	--

⊗

XX

XX

PR 16-SEP-1998; 98US-0100598P.

PR 16-SEP-1998; 98US-0100625P.

PA (VITA-) VITAGENIX INC.

PI Seifert W;

DR WPI; 2000-271267/23.

PT New antisense oligonucleotide

PT RNA sequence in bacteria.

PS Claim 10; Page 29; 50pp; Eng

CC This sequence represents an a

CC The invention relates to anti-

CC sequence in a bacterium. The

CC proteins, ribosomal RNA, ribosomal proteins, proteins essential for
CC nutrient uptake, proteins associated with pathogenicity, subunits of DNA-
CC dependent RNA polymerase, and DNA polymerase. The antisense

CC oligonucleotides are used to treat or diagnose bacterial infections
 XX Sequence 16 BP; 4 A; 3 C; 4 G; 5 T; 0 U; 0 Other;
 SQ

Query Match 2.3%; Score 14; DB 3; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 417 GACCTTCAAGATT 430
 |||||
 Db 16 GACCTTCAAGATT 3

RESULT 4
 AAA20709
 ID AAA20709 standard; RNA; 17 BP.
 AC AAA20709;
 XX
 DT 19-JUN-2000 (first entry)

DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3935.
 XX
 XX

Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; AMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberculous scleritis; pot-wine stain; Sturge Weber syndrome;
 KW Kippen-Treanunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.
 OS
 XX WO9950403-A2.
 PN
 XX 07-OCT-1999.
 PD
 XX 24-MAR-1999; 99WO-US006507.
 PF
 XX 27-MAR-1998; 98US-0079678P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA

PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA;
 XX
 XX WPI; 1999-591315/50.
 DR

PT Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 XX

PS Claim 55; Page 162; 305pp; English.

XX The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a TIE-2 gene. AA16775 to
 CC AA17167 and AA17561 to AA17622 represent ribozyme sequences for ARNT,
 CC and AA17168 to AA17560 and AA17623 to AA17684 represent the ARNT,
 CC corresponding target sequences; AA17685 to AA18385 and AA19087 to
 CC AA19134 represent ribozyme sequences for TIE-2, and AA18386 to AA19086
 CC and AA19135 to AA19222 represent their corresponding target sequences;
 CC AA19223 to AA20361 and AA21501 to AA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AA20362 to AA21500 and
 CC AA21596 to AA21688 represent their corresponding target sequences;
 CC AA21689 to AA22475 and AA23263 to AA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AA22476 to AA23262, AA23343 to
 CC AA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or TIE-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related

CC macular degeneration (AMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberculous scleritis, pot-wine stain, Sturge Weber
 CC syndrome, Kippen-Treanunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, TIE-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX

SQ Sequence 17 BP; 8 A; 3 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 2.3%; Score 14; DB 2; Length 17;
 Best Local Similarity 78.6%; Pred. No. 1.2e+04;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 37 TACCAATCAAAA 50
 :|||:
 Db 1 UACCAATCAAAA 14

RESULT 5
 ABT34570
 ID ABT34570 standard; DNA; 17 BP.
 XX
 XX ABT34570;
 AC
 XX 12-JUN-2003 (first entry)

DT Tumour suppression related human fukutin oligo SEQ ID No 207.
 XX
 XX

Cytostatic; vinorelbine; neuroprotective; neurotropic; neuroleptic; gene chip;
 KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizoprenia; protein chip; gene therapy; tumour suppression;
 KW human fukutin; ds.
 KW
 XX

XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-1B004208.
 PF
 XX 17-SEP-2001; 2001PR-00011978.
 PR
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA

PI Teletman A, Amson R, Tuijnder M;
 XX
 XX WPI; 2003-313353/30.
 DR

PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 XX

PS Disclosure; Page 58; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterised by development of tumours or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizoprenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and

CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 2 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 2.3%; Score 14; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 247 TCCTGGAGCCCTG 260
DB 3 TCCTGGAGCCCTG 16
RESULT 6
ADB42497
ID ADB42497 standard; DNA; 17 BP.
XX
AC ADB42497;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2820.
XX
KM cytostatic; antiviral; neuroprotective; nocrotic; neuroleptic; ss;
KM primer; probe; tumour suppression; tumour reversion; apoptosis;
KM virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KM diagnosis.
XX
OS Homo sapiens.
XX
PN MO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002MO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Teletman A, Amson R, Twijnder M;
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen.
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX
PS Disclosure; Page 361; 771pp; French.
XX
XX The invention relates to the isolation of 6327 nucleotide sequences.
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal

CC expression of the nucleotides.
XX
SQ Sequence 17 BP; 6 A; 2 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 2.3%; Score 14; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 422 TCAAGATTATTT 435
DB 3 TCAAGATTATTT 16
RESULT 7
AAV09174
ID AAV09174 standard; DNA; 20 BP.
XX
AC AAV09174;
XX
DT 09-JUN-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide sequence 8051 targeting ILIR mRNA.
XX
XX Type I interleukin-1 receptor; ILIR; human; ILI protein; hybridisation;
XX inflammation; ss; 5' Cap region; phosphorothioate linkage.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
XX
XX MO9744656-A1.
XX
XX 27-NOV-1997.
XX
XX 12-MAY-1997; 97MO-US007147.
XX
XX 21-MAY-1996; 96US-00651692.
XX
XX (ISIS-) ISIS PHARM INC.
XX
PI Miraglia L, Bennett CF, Dean N, Geiger T;
XX
XX WPI; 1998-018646/02.
XX
XX 2'-substituted oligonucleotide(s) specific for interleukin-1 receptor
XX type I - used to modulate expression and detect overexpression of the
XX receptor.
XX
XX Example 5; Page 19; 63pp; English.
XX
XX This is a novel oligomer comprising 20 covalently linked nucleotides
CC which bind to the 5' Cap region of the interleukin-1 receptor (ILIR)
CC mRNA. Expression of ILIR, in cells and tissues can be modulated by
CC compositions comprising oligomers which are able to specifically
CC hybridise with target areas of its encoding sequence. The composition can
CC be used for treatment of disease in humans caused by excessive receptor
CC expression, e.g. inflammation. When labelled they can be used
CC diagnostically to determine overexpression of ILIR, also to determine
CC localisation and distribution of this expression for research, diagnostic
CC or therapeutic purposes
XX
SQ Sequence 20 BP; 1 A; 8 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 2.3%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 373 GGAGTGGCGGCT 386
|||||

DT	10-JUL-2003	(first entry)
DE	Novel human protein identification related primer #13.	
KW	Human; cytostatic; DAPK3-Agonist; DAPK3-Antagonist; cancer; NOV; PCR; primer; ss.	
XX	Homo sapiens.	
XX	MO2003031571-A2.	
XX	17-APR-2003.	
XX	02-OCT-2002; 2002MO-US031357.	
XX	05-OCT-2001; 2001US-0327454P.	
XX	09-OCT-2001; 2001US-0327917P.	
XX	09-OCT-2001; 2001US-0328029P.	
XX	09-OCT-2001; 2001US-0328056P.	
XX	12-OCT-2001; 2001US-0328849P.	
XX	15-OCT-2001; 2001US-0329414P.	
XX	17-OCT-2001; 2001US-0330142P.	
XX	22-OCT-2001; 2001US-0341058P.	
XX	24-OCT-2001; 2001US-0343629P.	
XX	29-OCT-2001; 2001US-0349575P.	
XX	01-NOV-2001; 2001US-0346357P.	
XX	25-JUN-2002; 2002US-0391342P.	
XX	01-OCT-2002; 2002US-00262445.	
PA	(CURA-) CURAGEN CORP.	
XX	Alcobrook JP, Burgess CE, Catterton E, Chant JS, Chaudhuri A,	
PI	Edinger SR, Gerlach VL, Giot L, Gorman M, Guo X, Kexuda R,	
PI	Mezes PS, Millet I, Ooi CE, Patturajan M, Rieger DK, Spytek KA,	
PI	Taupier RJ, Zernhuseu BD, Zhong H, Zhong M,	
XX	WPI; 2003-381704/36.	
DR	New DAPK3 polypeptide, useful for preparing a composition for treating or	
PT	preventing e.g., cancer.	
XX	Example 20C; Page 212; 253pp; English.	
PS	The invention describes an isolated polypeptide comprising any of 33 90-	
CC	1273 amino acid sequences (1) given in the specification or its mature	
CC	form, a sequence that is at least 95 % identical to (1), or a sequence	
CC	comprising one or more conservative substitutions in the amino acid	
CC	sequence of (1). The polypeptide is useful for preparing a composition	
CC	for treating or preventing e.g. cancer. This sequence represents a primer	
CC	used to isolate DNA encoding a novel human NOV protein	
CC	SEQ	
XX	Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;	
QY	Query Match 2.3%; Score 14; DB 7; Length 20;	
XX	Best Local Similarity 100.0%; Pred.No. 1.2e+04;	
XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX	551 ATGAGGTTGATGAC 564	
XX	1 ATGAGGTTGATGAC 14	
XX	RESULT 11	
XX	ADC26512	
XX	ADC26512 standard; DNA; 20 BP.	
XX	ADC26512;	
XX	18-DEC-2003 (first entry)	
XX	NOV protein-related forward PCR primer SEQ ID 337.	
XX	NOV; cytostatic; metabolic disorder; immune; neurodegenerative;	

KM	circulatory; haemopoietic; wasting; cancer; gene therapy; vaccine;
XW	transgenic; human; ss; PCR; primer.
XX	
OS	Homo sapiens.
PN	M02003004687-A2.
XX	
PD	16-JAN-2003.
XX	
PJ	03-JUL-2002; 2002WO-US021361.
XX	
PR	05-JUL-2001; 2001US-0303046P.
PR	09-JUL-2001; 2001US-0303828P.
PR	09-JUL-2001; 2001US-0304016P.
PR	11-JUL-2001; 2001US-0304502P.
PR	13-JUL-2001; 2001US-0305262P.
PR	16-JUL-2001; 2001US-0305673P.
PR	17-JUL-2001; 2001US-0306085P.
PR	24-JUL-2001; 2001US-0307356P.
PR	27-JUL-2001; 2001US-0308228P.
PR	30-JUL-2001; 2001US-0308877P.
PR	01-AUG-2001; 2001US-0309255P.
PR	17-AUG-2001; 2001US-031338P.
PR	12-SEP-2001; 2001US-0318711P.
PR	19-SEP-2001; 2001US-0323380P.
PR	21-SEP-2001; 2001US-0323699P.
PR	04-OCT-2001; 2002US-0345022P.
PR	04-FEB-2002; 2002US-0345038P.
PR	28-FEB-2002; 2002US-0361172P.
PR	01-MAR-2002; 2002US-0360814P.
PR	01-MAR-2002; 2002US-0360830P.
PR	01-MAR-2002; 2002US-0361133P.
PR	01-MAR-2002; 2002US-0361147P.
PR	05-MAR-2002; 2002US-0361677P.
PR	02-APR-2002; 2002US-0363637P.
PR	12-APR-2002; 2002US-0372336P.
PR	16-APR-2002; 2002US-0372950P.
PR	19-APR-2002; 2002US-0373881P.
PR	19-APR-2002; 2002US-0373921P.
PR	02-JUL-2002; 2002US-00188186.
PA	(CURA-) CURAGEN CORP.
PI	Anderson DM, Bergis C, Boldog FL, Burgess CE, Casman SJ,
PI	Catterton E, Edinger S, Eisen AJ, Ellemann K, Gerlach V, Gorman L,
PI	Guo X, Jeffers M, Kekuda R, Li L, Malvankar UM, Miller CE,
PI	Padigan M, Patturajan M, Pena CB, Ratelli L, Shenoy S,
PI	Shinkels RA, Spaderna SK, Spytek KA, Stone DT, Taupier RJ,
PI	Vernet CM, Voss EZ, Zhong M;
DR	WPI; 2003-221607/21.
PT	New isolated NOVX polypeptide, useful for determining the presence of, or
PT	predisposition to a disease associated with altered levels of expression
PT	of the polypeptide, and for treating or preventing cancer.
PS	Example C; SEQ ID NO 337; 478bp; English.
CC	The invention relates to a novel isolated NOV polypeptide. The
CC	polypeptide of the invention demonstrates cytostatic activity and may be
CC	used for determining the presence of, or predisposition to a disease
CC	associated with altered levels of expression of the polypeptide,
CC	including metabolic disorders, immune disorders, neurodegenerative
CC	disorders, circulatory diseases, haemopoietic disorders, wasting diseases
CC	and cancer. The polypeptide may also be utilised during gene therapy
CC	procedures, vaccine development and transgenic animal production. The
CC	current sequence is that of the PCR primer of the invention which was
CC	used to analyse human NOV DNA.
SC	Sequence 20 BP; 2 A; 6 C; 5 G; 7 T; 0 U; 0 Other;
Query Match	2.3%; Score 14; DB 9; Length 20;
Best Local Similarity	100.0%; Pred No. 1.2e+04;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 258 CTGCTACGACTGNG 271
 |||||
 Db 6 CTGCTACGACTGTG 19

RESULT 12

ABT05327
 ID ABT05327 standard; DNA; 15 BP.

AC ABT05327;
 ATGCTCTTCTCTC 186

DT 24-OCT-2002 (first entry)

DE Human N-acetylglactosaminidase (NAGA) alpha gene ASO primer 19.

KM Human; PCR; primer; ss; gene therapy; N-acetylglactosaminidase alpha;
 KM chromosome 22q13.2-q13.31; lysosomal glycosidase; screening; SNP;
 KM NAGA-related disease; single nucleotide polymorphism; haplotyping; NAGA;
 KM genotyping.

OS Homo sapiens.

PN WO200194637-A1.

PD 13-DEC-2001.

PF 07-JUN-2001; 2001WO-US018456.

PR 07-JUN-2000; 2000US-0210110P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Duda A, Kazemi A, Kosny B, Parks KE;

DR WPI; 2002-566449/60.

PT New genetic variants of isolated N-acetylglactosaminidase (NAGA), Alpha
 PT gene, useful for therapeutic purposes, for studying the expression and
 PT function of the polymorphic site, and for expressing NAGA protein.

PS Claim 16; Page 13; 91pp; English.

CC The invention comprises the amino acid and coding sequence of the human N
 CC -acetylglactosaminidase (NAGA) alpha protein. The invention specifically
 CC comprises novel polymorphic sites identified within the NAGA gene. The
 CC NAGA gene is located on chromosome 22q13.2-q13.31 and encodes a
 CC lysosomal glycosidase that cleaves alpha-N-acetylglactosaminyl
 CC moieties in glycoconjugates. The NAGA DNA and protein sequences of the
 CC invention are useful for studying the expression and function of NAGA and
 CC for screening candidate drugs to treat diseases related to NAGA activity.
 CC The NAGA gene polymorphisms identified in the present invention are
 CC useful for haplotyping and genotyping the NAGA gene of an individual. The
 CC present DNA sequence represents an N-acetylglactosaminidase gene allele-
 CC specific oligonucleotide primer

XX Sequence 15 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 1 Other;

Qy Query Match 2.2%; Score 13; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 174 ATTGCTCTTCTCTC 186
 |||||
 Db 1 ATTGCTCTTCTCTC 13

RESULT 13

ABK24744
 ID ABK24744 standard; DNA; 17 BP.

XX ABK24744;
 AC ABK24744;

XX 09-APR-2002 (first entry)

DE Glycosate resistance conferring genome altering oligonucleotide #104.

XX Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KM o-methyl modification; LNA modification; phosphorothioate linkage;
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KM abiotic stress tolerance; improved nutritional value; hygromycin-B;
 KM amino acid over production; herbicide resistance; glyphosate resistance;
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;
 KM modified oil production; modified starch production; waxy starch;
 KM altered floral morphology; male-sterile plant; albino mutant;
 KM modified fatty acid content; reduced palmitate production; albino plant;
 KM increased stearate production; reduced linoleic acid production;
 KM photosynthetic process.

OS Hordeum vulgare.

PN WO200192512-A2.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-US017672.

PR 01-JUN-2000; 2000US-0208538P.

PR 30-OCT-2000; 2000US-0244889P.

PR 27-MAR-2001; 2001US-00818875.

PA (UYDE) UNIV DELAWARE.

PI Kmlec EB, Gamper HB, Rice MC, Kim J;

DR WPI; 2002-106307/14.

PT New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.

PS Claim 7; Page 51; 220pp; English.

CC The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).
 CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention

XX Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Qy Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 70 CGCGGTGAGACCT 82
 DB 2 CGCGGTGAGACCT 14
 RESULT 14
 ID ABRK24743/c
 AC ABRK24743 standard; DNA; 17 BP.
 DT 09-APR-2002 (first entry)
 XX
 XX
 DE Glycosate resistance conferring genome altering oligonucleotide #103.
 KM Chromosomal genomic alteration; genome altering oligonucleotide; PCR; ss;
 KM o-methyl modification; LNA modification; phosphorothioate linkage;
 KM DNA repair; DNA alteration; environmental tolerance; hygromycin-B;
 KM abiotic stress tolerance; improved nutritional value; hygromycin; primer;
 KM amino acid over production; herbicide resistance; glyphosate resistance;
 KM imidazolinone herbicide resistance; sulphonylurea herbicide resistance;
 KM porphyrin herbicide resistance; triazine resistance; disease resistance;
 KM modified oil production; modified starch production; waxy starch;
 KM altered floral morphology; male-sterile plant; albino mutant;
 KM modified fatty acid content; reduced palmitate production; albino plant;
 KM increased stearate production; reduced linoleic acid production;
 KM photosynthetic process.
 OS Hordeum vulgare.
 OS Synthetic.
 PN WO200192512-A2.
 PD 06-DEC-2001.
 XX
 XX 01-JUN-2001; 2001WO-US017672.
 PF
 XX 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 PR 27-MAR-2001; 2001US-00818875.
 XX
 XX (UNDE) UNIV DELAWARE.
 PA Kmiec EB, Gampier HB, Rice MC, Kim J;
 PI WPI; 2002-106307/14.
 DR
 XX
 XX New oligonucleotides with modified nuclease-resistant termini, useful for
 PT creating plants with desired phenotypes, e.g. stress tolerance, improved
 PT nutritional value, herbicide or disease resistance, or modified oil
 PT production.
 PS Claim 7; Page 51; 220pp; English.
 XX
 XX The invention relates to an oligonucleotide for targeted alteration of a
 CC genetic sequence, which comprises a single-stranded oligonucleotide
 CC having a DNA domain. The DNA domain has at least one mismatch with
 CC respect to the genetic sequence to be altered and further comprises
 CC chemical modifications of the oligonucleotide. The chemical modifications
 CC consist of o-methyl modification, an LNA modification, two or more
 CC phosphorothioate linkages on a terminus, or a combination of any two or
 CC more of these modifications. The oligonucleotides are useful for
 CC directing repair or alteration of plant genetic information. The
 CC oligonucleotides are particularly useful for creating plants with desired
 CC phenotypes, e.g. environmental or abiotic stress tolerance, improved
 CC nutritional value (e.g. altering amino acid content of plants or
 CC conferring amino acid over production), herbicide resistance (e.g.
 CC glyphosate resistance, imidazolinone and sulphonylurea herbicide
 CC resistance, porphyrin herbicide resistance or triazine resistance),
 CC disease resistance, modified oil production, modified starch production
 CC (e.g. increased starch or production of waxy starch), altered floral
 CC morphology (e.g. male-sterile plants) or modified fatty acid content
 CC (e.g. reduced palmitate, increased stearate or reduced linoleic acid).

CC The oligonucleotides are also useful for producing albino mutants for the
 CC analysis of photosynthetic processes. This sequence represents a genome
 CC altering oligonucleotide of the invention
 XX
 XX Sequence 17 BP; 2 A; 8 C; 5 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Fred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 70 CGCGGTGAGACCT 82
 DB 16 CGCGGTGAGACCT 4
 RESULT 15
 ID ABRV79549/c
 AC ABRV79549 standard; DNA; 17 BP.
 XX
 XX ABRV79549;
 AC
 XX 03-JAN-2003 (first entry)
 DT
 XX
 DE Human HTPL scanning oligonucleotide SEQ ID 795.
 XX
 XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KM human testis expressed Patched like protein; testis; adrenal; liver;
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 OS EP1229046-A2.
 PN
 XX 07-AUG-2002.
 PD
 XX 28-JAN-2002; 2002EP-00001167.
 PF
 XX 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 XX (AEOM-) AEOMICA INC.
 PA Zhan J;
 PI WPI; 2002-676582/73.
 DR
 XX
 XX Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.
 PS Example 2; Page 168; 718pp; English.
 XX
 XX The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABRV78759 to ABRV78762 and ABR88519 to ABR88520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-8 (S for short) compared to HTPL-1 (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and

CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
 Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 385 CTGCACCGCGCCG 397
 DB 17 CTGCACCGCGCCG 5
 RESULT 16
 ABV79553/c
 ID ABV79553 standard; DNA; 17 BP.
 AC ABV79553;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPPL scanning oligonucleotide SEQ ID 799.
 XX
 KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
 KM human testis expressed Patched like protein; testis; adrenal; liver;
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 PT Novel isolated human testis expressed Patched like protein (HTPPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPPL.
 XX
 PS Example 2; Page 168; 718pp; English.
 XX
 PS The present invention relates to human testis expressed Patched like
 CC protein (HTPPL, see ABV78759 to ABV78762 and AB998519 to AB998520). HTPPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is
 CC important in regulating male germ cell development, and the HTPPL gene was
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of

CC such disorder associated with decreased expression or activity of human
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
 Query Match 2.2%; Score 13; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 385 CTGCACCGCGCCG 397
 DB 13 CTGCACCGCGCCG 1
 RESULT 17
 ABV79551/c
 ID ABV79551 standard; DNA; 17 BP.
 AC ABV79551;
 XX
 DT 03-JAN-2003 (first entry)
 XX
 DE Human HTPPL scanning oligonucleotide SEQ ID 797.
 XX
 KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;
 KM human testis expressed Patched like protein; testis; adrenal; liver;
 KM male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KM prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI229046-A2.
 XX
 PD 07-AUG-2002.
 XX
 PF 28-JAN-2002; 2002EP-00001167.
 XX
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 09-OCT-2001; 2001US-0327898P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Zhan J;
 XX
 DR WPI; 2002-676582/73.
 XX
 PT Novel isolated human testis expressed Patched like protein (HTPPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPPL.
 XX
 PS Example 2; Page 168; 718pp; English.
 XX
 PS The present invention relates to human testis expressed Patched like
 CC protein (HTPPL, see ABV78759 to ABV78762 and AB998519 to AB998520). HTPPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is
 CC important in regulating male germ cell development, and the HTPPL gene was
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are

CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 9 G; 1 T; 0 U; 0 Other;

CC Query Match 2.2%; Score 13; DB 6; Length 17;

CC Best Local Similarity 100.0%; Pred. No. 3.8e+04;

CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCCG 397

DB 15 CTGCACCGCGCCG 3

RESULT 18

ABV79552/c

ID ABV79552 standard; DNA; 17 BP.

XX AC ABV79552;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPPL scanning oligonucleotide SEQ ID 798.

XX KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

XX KM human testis expressed Patched like protein; testis; adrenal; liver;

XX KM male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KM prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX PT WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPPL.

CC important in regulating male germ cell development, and the HTPPL gene was
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

XX SQ Sequence 17 BP; 3 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

CC Query Match 2.2%; Score 13; DB 6; Length 17;

CC Best Local Similarity 100.0%; Pred. No. 3.8e+04;

CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCCG 397

DB 14 CTGCACCGCGCCG 2

RESULT 19

ABV79550/c

ID ABV79550 standard; DNA; 17 BP.

XX AC ABV79550;

XX DT 03-JAN-2003 (first entry)

XX DE Human HTPPL scanning oligonucleotide SEQ ID 796.

XX KM Human; gene therapy; tumour suppressor; HTPPL; chromosome 10p12.1;

XX KM human testis expressed Patched like protein; testis; adrenal; liver;

XX KM male germ cell development; bone marrow; brain; kidney; lung; placenta;

XX KM prostate; skeletal muscle; colon; male infertility; cancer; ss.

XX OS Homo sapiens.

XX PN EP1229046-A2.

XX PD 07-AUG-2002.

XX PF 28-JAN-2002; 2002EP-00001167.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 23-MAY-2001; 2001US-00864761.

XX PR 09-OCT-2001; 2001US-0327898P.

XX PA (AEOM-) AEOMICA INC.

XX PI Zhan J;

XX PT WPI; 2002-676582/73.

XX PT Novel isolated human testis expressed Patched like protein (HTPL), useful

XX PT for identifying agonist and antagonist and specific binding partners, and

XX PT for treating subjects having defects in HTPPL.

XX PS Example 2; Page 168; 718pp; English.

XX PS The present invention relates to human testis expressed Patched like

XX PS protein (HTPL), see ABV78759 to ABV78762 and AB898519 to AB898520). HTPPL

XX PS has two isoforms, with a few single base pair differences between the

XX PS two. One of the single base pair changes introduces a premature stop

XX PS codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL

XX PS shares an overall structure organisation with the Patched protein. The

XX PS codon in HTPPL-S (S for short) compared to HTPPL-L (L for long). HTPPL

XX PS shares an overall structure organisation with the Patched protein. The

CC shared structural features strongly imply that HTPPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPPL is
 CC important in regulating male germ cell development, and the HTPPL gene was
 CC mapped to human chromosome 10p12.1. HTPPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention

SO Sequence 17 BP; 2 A; 4 C; 10 G; 1 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 CTGCACCGCGCGG 397

DB 16 CTGCACCGCGCGG 4

RESULT 20

ABL31517

ID ABL31517 standard; DNA; 17 BP.

AC ABL31517;

DT 21-MAR-2002 (first entry)

DE Human HLA genotyping oligonucleotide SEQ ID NO 1006.

XX Human; human leukocyte antigen; HLA; genotype; polymorphism;

XX immunogenetic; transplantation; genetic disease; ss.

OS Homo sapiens.

PN WO200192572-A1.

PD 06-DEC-2001.

PF 01-JUN-2001; 2001WO-0P004662.

PR 01-JUN-2000; 2000JP-00164798.

PA (NISON) NISSHINBO IND. INC.

PA (SYST-) SYSTEM RES INC.

PI Inoko H, Kagiya T, Ichihara T, Matsumura Y, Moriya S, Nishida M;

PI WPI; 2002-122074/16.

PT Human leukocyte antigen (HLA) typing, useful for judging HLA genotypes of

PT individuals e.g. by determining immunogenetic differences when

PT transplanting between them.

PS Claim 10; Page 284; 345pp; Japanese.

XX The invention relates to a typing kit for judging human leukocyte antigen

CC (HLA) genotype of a sample by hybridising a substrate on which 10-24 base

CC oligonucleotides (ABL30512-ABL31809) originating in the sequences of

CC genes e.g. belonging to HLA class I antigens on human genome and

CC containing gene polymorphisms as allantoic acids have been immobilised as

CC primers for amplification of cleaved nucleic acids relating to gene

CC polymorphisms. The method is useful for judging HLA genotypes of

CC individuals by determining immunogenetic differences before transplanting

CC organ and tissue for transplantation e.g. of bone marrow, kidney, liver,

CC pancreas, Langerhans islet in pancreas and cornea, susceptibility

CC diagnosis of genetic diseases and identifying individuals

XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

SO Query Match 2.2%; Score 13; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 GGCTGCCACCTGG 172

DB 3 GGCTGCCACCTGG 15

RESULT 21

ACC53277

ID ACC53277 standard; DNA; 17 BP.

AC ACC53277;

DT 27-JUN-2003 (first entry)

DE Human tumour suppressor sequence #2044.

XX ss; tumour suppressor; antitumour; cytoskeletal; tumour suppression;

XX tumour regression; apoptosis; virus resistance; diagnosis;

XX cellular degeneration.

OS Homo sapiens.

PN FR2826373-A1.

PD 27-DEC-2002.

PF 20-JUN-2001; 2001FR-00008139.

PR 20-JUN-2001; 2001FR-00008139.

PA (MOLE-) MOLECULAR ENGINES LAB SA.

PI Tufjander M, Telerman A, Amson R;

PI WPI; 2003-250498/25.

PT New nucleic acid sequences associated with tumor suppression, regression,

PT apoptosis or virus resistance are useful to diagnose and treat viral

PT disease, development of tumor cells and cell degeneration.

PS Claim 1; Page 512; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated

CC with tumour suppression or regression, apoptosis or virus resistance. The

CC invention relates to these sequences or sequences having at least 80%

CC identity to them, and polypeptides encoded by the sequences or

CC polypeptides having 80% identity to the polypeptide sequences. The

CC invention is used to diagnose or treat viral disease or disease

CC characterized by development of tumour cells or cellular degeneration

SO Sequence 17 BP; 4 A; 4 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATCCTTTTCACTG 132

DB 2 ATCCTTTTCACTG 14

RESULT 22

ADA9326/c

ID ADA9326 standard; DNA; 17 BP.

AC ADA9326;

XX


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XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 316; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
XX Query Match      2.2%; Score 13; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      246 CTCCTGGAGCCCC 258
XX      |||||
XX      14 CTCCTGGAGCCCC 2
XX
XX Db
XX
XX RESULT 25
XX ADA9324/c
XX ID ADA9324 standard; DNA; 17 BP.
XX AC ADA9324;
XX ADADA9324;
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MD23 scanning oligonucleotide SEQ ID 313.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX

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XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 313; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic loci. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 3 A; 3 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match      2.2%; Score 13; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.8e+04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY      246 CTCCTGGAGCCCC 258
XX      |||||
XX      17 CTCCTGGAGCCCC 5
XX
XX Db
XX
XX RESULT 26
XX ADA9328/c
XX ID ADA9328 standard; DNA; 17 BP.
XX AC ADA9328;
XX ADADA9328;
XX DT 20-NOV-2003 (first entry)
XX
XX DE Human MD23 scanning oligonucleotide SEQ ID 317.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EPI281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 317; 103pp; English.
XX

```

CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC alterations can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.

SQ Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 246 CTCCTGAGCCCC 258
13 CTCCTGAGCCCC 1

DB 13 CTCCTGAGCCCC 1

RESULT 27
ABZ61946/c
ID ABZ61946 standard; RNA; 17 BP.
XX
XX ABZ61946;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human H-Ras DNAzyme target #737.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX MCSwigen J;
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX MCSwigen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

PS Claim 58; Page 125; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,

CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

SQ Sequence 17 BP; 1 A; 6 C; 5 G; 0 T; 5 U; 0 Other;

Query Match 2.2%; Score 13; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 GCAAGGCTGAGCC 368
15 GCAAGGCTGAGCC 3

DB 15 GCAAGGCTGAGCC 3

RESULT 28
ABZ61384
ID ABZ61384 standard; RNA; 17 BP.
XX
XX ABZ61384;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human H-Ras DNAzyme target #175.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosolic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX MCSwigen J;
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX 06-JUN-2001; 2001US-0296249P.
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX MCSwigen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

PS Claim 58; Page 114; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytosolic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ5989 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention

SQ Sequence 17 BP; 0 A; 5 C; 11 G; 0 T; 1 U; 0 Other;

Query Match 2.2%; Score 13; DB 7; Length 17;
Best Local Similarity 92.3%; Pred. No. 3.8e+04;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 372 GGGGCTGCGCGG 384
 |||||
 DB 3 GGGGCTGCGCGG 15

RESULT 29
 AA24774/C
 ID AA24774 standard; DNA; 18 BP.

AC AA24774;

DT 19-APR-2000 (first entry)

DE Human FADD primer ISIS #23874.

KM FADD; human; antisense; inhibitor; Fas-associated death domain; primer;
 KW probe; ss.

OS Homo sapiens.

PN US6015712-A.

PD 18-JAN-2000.

PF 19-JUL-1999; 99US-00357072.

PR 19-JUL-1999; 99US-00357072.

PA (ISIS-) ISIS PHARM INC.

PI Mona BP, Cowser LM, Baker BF, Zhang H;

DR WPI; 2000-126316/11.

PT Antisense oligonucleotides, useful for inhibiting human Fas-associated
 death domain (FADD) expression are targeted to the 3' untranslated region
 of the FADD gene.

PS Example 16; Col 53-54; 37pp; English.

CC This invention describes novel antisense oligonucleotides (OGNs) (I) 8-20
 CC nucleotides in length that specifically hybridize with and inhibit
 CC nucleic acids encoding human Fas-associated death domain (FADD), targeted
 CC to the 3' untranslated region (3'UTR). (I) can be used to treat animals,
 CC especially humans, suspected of having or being prone to a disease or
 CC condition associated with FADD expression. AA24746-244831 represent
 CC primers and probes used in the method of the invention

SQ Sequence 18 BP; 6 A; 5 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 130 CTGGACTTTGGTT 142
 |||||

DB 14 CTGGACTTTGGTT 2

RESULT 30
 AA241855/C
 ID AA241855 standard; cDNA; 19 BP.

AC AA241855;

DT 21-FEB-1997 (first entry)

DE Probe/primer for Plasmodium falciparum erythrocyte membrane protein.

KM Plasmodium falciparum; erythrocyte membrane protein; malaria; detection;
 KW identification; treatment; prevention; parasite; ss.

OS Synthetic.

XX W09633736-A1.

XX 31-OCT-1996.

XX 26-APR-1996; 96WO-US005798.

XX 27-APR-1995; 95US-00430908.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Baruch DI, Pasloske BL, Howard RJ;

XX WPI; 1996-497376/49.

PT New Plasmodium falciparum erythrocyte membrane proteins - used to develop
 products for the diagnosis, treatment or prevention of malaria parasite
 infections.

PS Disclosure; Page 24; 149pp; English.

CC A polypeptide comprising a Plasmodium falciparum (Pf) erythrocyte
 CC membrane protein 1 (PfEMP1) or active fragments or analogues of that
 CC protein can be used in the treatment or prevention of symptoms of a
 CC malaria parasite infection. The polypeptides can inhibit, block or
 CC reverse the sequestration of erythrocytes in patients suffering from
 CC malaria. Nucleic acids derived from the PfEMP1 gene can be used as probes
 CC and primers to identify a Plasmodium falciparum parasite, the primers
 CC used to generate characteristic amplification patterns from different P.
 CC falciparum strains. Antibodies specifically immunoreactive with the
 CC PfEMP1 polypeptide or its fragments may be used in diagnosis of malaria
 CC infection. Nucleic acid fragments of at least 15 contiguous nucleotides
 CC of the PfEMP1 gene are also claimed. They may be generated by
 CC amplification with the probes/primers described in AA241854-741867

SQ Sequence 19 BP; 8 A; 2 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 508 GTTCGCTCTCCA 520
 |||||

DB 15 GTTCGCTCTCCA 3

RESULT 31
 AA283045/C
 ID AA283045 standard; DNA; 19 BP.

AC AA283045;

DT 04-DEC-2000 (first entry)

DE cdk6 ribozyme binding site #105.

KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

PN W0200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

PA (IMMU-) IMMUSOL INC.

XX Tritz R, Welch PJ, Barber JR, Robbins JM;

XX WPI; 2000-412314/35.

XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 55; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
Query Match 2.2%; Score 13; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 481 GCCTGGAGAGGC 493
DB 17 GCCTGGAGAGGC 5
RESULT 32
AAA83046/c
ID AAA83046 standard; DNA; 19 BP.
XX AC AAA83046;
XX DT 04-DEC-2000 (first entry)
XX DE cdk6 ribozyme binding site #106.
XX KM Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX OS Mammalia.
XX PN WO200032765-A2.
XX PD 08-JUN-2000.
XX PF 06-DEC-1999; 99WO-US028772.
XX PR 04-DEC-1998; 98US-0110954P.
XX PA (IMMU-) IMMUSOL INC.
XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX DR WPI; 2000-412314/35.
XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX PS Disclosure; Page 55; 109pp; English.
XX CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX SQ Sequence 19 BP; 2 A; 7 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 2.2%; Score 13; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 481 GCCTGGAGAGGC 493
DB 16 GCCTGGAGAGGC 4
RESULT 33
AA165672/c
ID AA165672 standard; DNA; 19 BP.
XX AC AA165672;
XX DT 03-JAN-2002 (first entry)
XX DE Primer for studying biallelic polymorphic markers in the IBD1 region.
XX KM Human; inflammatory bowel disease 1 protein; IBD1; IBD1prox;
KM intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;
KM inflammatory disease; immune disease; cryptogenic inflammation;
KM hemorrhagic rectocolitis; Crohn's disease; Blau syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX PN FR2806739-A1.
XX PD 28-SEP-2001.
XX PF 27-MAR-2000; 2000FR-00003832.
XX PR 27-MAR-2000; 2000FR-00003832.
XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.
XX PI Hugot JP, Thomas G, Zouali M, Lesage S, Chamaillard M;
XX DR WPI; 2001-608364/70.
XX PT New human nucleic acids associated with intestinal inflammatory disease,
PT useful for diagnosis, prognosis and control of these diseases, also
PT related proteins.
XX PS Example 4; Page 88; 97pp; French.
XX CC Primers AA165647-78 were used to characterise biallelic polymorphic
CC markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory
CC bowel disease 1 (IBD1) polypeptide, which is associated with intestinal
CC inflammatory disease. The specification also describes a polypeptide
CC which is in proximity to IBD1, and is designated IBD1prox. The IBD1 gene
CC is probably involved in regulation of apoptosis and activation of NF-
CC kappa B. The IBD1 and IBD1prox polynucleotides are useful as source of
CC probes and primers, as source of (anti)sense oligonucleotides, for
CC recombinant production of polypeptides, and in screening for interactive
CC compounds. The polypeptides are used to raise specific antibodies which
CC are useful for diagnostic detection or purification of IBD1 and IBD1prox, to
CC screen for specific binding agents, potential therapeutic agents. The
CC IBD1 and IBD1prox polynucleotides and polypeptides are useful for
CC treatment and prevention of inflammatory and/or immune diseases or
CC cancer, where associated with mutations in genes corresponding to IBD1
CC and IBD1prox, especially with mutations in genes corresponding to the intestines
CC (hemorrhagic rectocolitis, Crohn's disease and Blau syndrome)
XX SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 2.2%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 53 TCCGCTGGGCTAA 65
DB 18 TCCGCTGGGCTAA 6

XX	AAHS8207/c
XX	AAHS8207 standard; DNA; 19 BP.
XX	
AC	AAHS8207;
XX	
DT	10-SEP-2001 (first entry)
DE	Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:631.
XX	
KW	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW	recognition site; target; ribozyme binding site; eye disease; vulnerability;
KW	proliferative diseases; skin disease; psoriasis; diabetic retinopathy;
KM	cyclokin; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KM	matrix metalloproteinase; growth factor; reductase; scarring; cystostatic;
KM	antiproliferative; dermatological; antiseborrheic; antididiabetic; vitruide;
KM	antisclerotic; ophthalmological; keratolytic; gene therapy; viral wart;
KM	acopic dermatitis; actinic keratosis; squamous cell carcinoma;
KM	basal cell carcinoma; seboretheic wart; vitreoretinopathy; scar;
KM	sickle cell retinopathy; ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200130362-A2.
XX	
PD	03-MAY-2001.
XX	
PF	26-OCT-2000; 2000MO-USO29500.
PR	26-OCT-1999; 99US-0161532P.
PA	(IMMU-) IMMUSOL INC.
PL	Robbins JM, Tritz R;
DR	WPI; 2001-300427/31.
PT	Treating proliferative skin or eye diseases and scarring, using ribozymes
PT	that cleave RNA encoding cytokines involved in inflammation, matrix
FT	metalloproteinases, growth factors and cell-cycle dependent kinases.
XX	
PS	Example 1; Page 117; 408pp; English.
XX	
CC	The present invention describes a method for treating a proliferative
CC	skin or eye disease and scarring. The method involves administering a
CC	ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC	inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC	dependent kinase, growth factor or a reductase, or administering a
CC	nucleic acid molecule (II) comprising a promoter operably linked to a
CC	nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC	dermatological, cytotstatic, antiseborrheic, antididiabetic, antisickling,
CC	ophthalmological, vulnerary, keratolytic and vitruide activities, and
CC	cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC	in gene therapy. (I) and (II) are useful for treating proliferative skin
CC	diseases such as psoriasis, acopic dermatitis, actinic keratosis,
CC	squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC	also be used for treating proliferative eye diseases such as diabetic
CC	retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC	prematurity and retinal detachment, and for treating and preventing
CC	scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC	scar. AAHS7577 to AAHS2099 represent sequences used in the
XX	exemplification of the present invention
XX	
SD	Sequence 19 BP; 2 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

Query Match	2.2%;	Score 13;	DB 5;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 3.8e+04;		
Matches 13;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Db 17 GCCTGGGAAGGC 5

RESULT 35
AAH58208/c
ID AAH58208 standard; DNA; 19 BP.
XX
XX AAH58208;
DT 10-SEP-2001 (first entry)
DE Cell-cycle dependent kinase cdk6 ribozyme binding site SEQ ID NO:632.
XX
XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulvular;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cystostatic;
KW antiproliferative; dermatological; antiangiogenic; antidiabetic; vitricide;
KW anticaking; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborectheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; se.

XX Homo sapiens.
OS Synthetic.
XX
XX WC000130362-A2,
XX
XX PD 03-MAY-2001.
XX
XX 26-OCT-2000; 2000MO-USO29500.
XX
XX 26-OCT-1999; 99US-0161532P.
FR (IMMU-) IMMUSOL INC.
PA Robbins JM, Tritz R;
XX
XX WPI; 2001-300427/31.
DR

Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases.

Example 1; Page 118; 408bp; English.

The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or a reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antiproliferative, cytotoxic, cytostatic, angiobornetic, antidiabetic, anticaking, ophthalmological, vulvar, keratolytic and vincidine activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as psoriasis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborectheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing bearing such as keloid, adhesion and hypertrophic or hypertrophic burn soar. AAH57577 to AAH62099 represent sequences used in the exemplification of the present invention

SQ Sequence 19 BP; 2 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
 Query Match 2.2%; Score 13; DB 5; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.8e+4;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 481 GCCTGGAGAGGC 493
 DB 16 GCCTGGAGAGGC 4
 RESULT 36
 ACF03639/C
 ID ACF03639 standard; DNA; 19 BP.
 AC ACF03639;
 XX
 DT 15-SEP-2003 (first entry)
 XX
 DE Human NOV13 forward PCR primer SEQ ID NO:209.
 Human; NOVX; cytostatic; cardiac; anti-inflammatory; immunosuppressive;
 KM anti-angiogenic; haemostatic; anti-HIV; antidiabetic; antiatherosclerotic;
 KM anorectic; antiaesthetic; nephrotoxic; antitachytic; hepatocytic;
 KM neuroprotective; nootropic; antibacterial; virucide; antiparasitic;
 KM relaxant; anticonvulsant; hypotensive; vasotropic; antiparkinsonian;
 KM vulnery; angiogenic; antiangiogenic; gene therapy; vaccine; cancer;
 KM cardiomyopathy; atherosclerosis; hypertension; diabetes; inflammation;
 KM autoimmune disorder; allergy; blood disorder; AIDS; obesity; asthma;
 KM acquired immunodeficiency syndrome; nephropathy; cirrhosis; arthritis;
 KM Alzheimer's disease; Parkinson's disease; goitre; infection; stroke;
 KM muscular dystrophy; epilepsy; wasting disorder; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200294870-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 02-NOV-2001; 2001MO-US051580.
 XX
 PR 02-NOV-2000; 2000US-0245291P.
 PR 02-NOV-2000; 2000US-0245317P.
 PR 07-NOV-2000; 2000US-0246562P.
 PR 08-NOV-2000; 2000US-0246871P.
 PR 26-JAN-2001; 2001US-0264389P.
 PR 26-JAN-2001; 2001US-0264423P.
 PR 29-JAN-2001; 2001US-0264799P.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Grose WM, MacDougall JR, Smithson G, Miller I, Stone DJ;
 PI Gunter E, Ellerman K, Alsbrook JP, Lepley DM, Burgess CE;
 PI Szytek KA, Edinger SR, Gangoli EA, Gorman L, Taupier RJ, Li L;
 PI Guo X, Fernandes ER, Vernet CM, Tchervet VT, Casman SJ, Shenoy S;
 PI Mishra V, Furtak K, Baumgartner JC, Colman SD.
 DR WPI; 2003-140359/13.
 XX
 PT New NOVX polypeptide useful for preventing or treating NOVX-associated
 PT disorders, e.g. cancer, cardiomyopathy, atherosclerosis or diabetes, and
 PT in chromosome mapping, tissue typing or pharmacogenomics.
 XX
 PS Example 2, Page 316, 346pp; English.
 PS
 XX ACF03547 to ACF03570 encode the human NOVX proteins (I) given in AB57412
 CC to AB57435. (I) have cytostatic, cardiac, anti-inflammatory, nootropic,
 CC immunosuppressive, antiallergic, haemostatic, anti-HIV, antidiabetic,
 CC antiatherosclerotic, anorectic, antiaesthetic, nephrotoxic, virucide,
 CC antitachytic, hepatocytic, neuroprotective, antibacterial, relaxant,
 CC antiparkinsonian, anticonvulsant, hypotensive, vasotropic, antiparkinsonian,
 CC vulnery, angiogenic and antiangiogenic activities, and can be used in
 CC gene therapy and vaccines. The NOVX polypeptides and their antibodies can
 CC be used to determine the presence or absence of (I) in a sample. The NOVX
 CC polypeptides, polynucleotides encoding them, and antibodies against them,
 CC are useful in manufacturing a medicament for treating or preventing a
 CC syndrome associated with a NOVX-associated disorder such as hypertension,
 CC cardiomyopathy, atherosclerosis, cancer, diabetes, asthma, inflammation,

CC autoimmune disorders, allergies, blood disorders, obesity, acquired
 CC immunodeficiency syndrome (AIDS), immunoglobulin (Ig) A nephropathy,
 CC cirrhosis, arthritis, Alzheimer's disease, Parkinson's disease, goitre,
 CC infections (e.g. bacterial, viral, parasitic), stroke, muscular
 CC dystrophy, epilepsy, and other wasting disorders associated with chronic
 CC diseases. ACF03571 to ACF03644 represent PCR primers and probes for NOVX
 CC sequence, which are used in an example from the present invention
 XX
 SQ Sequence 19 BP; 5 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
 Query March 2.2%; Score 13; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 487 GAAGGCTGCATG 499
 DB 17 GAAGGCTGCATG 5
 RESULT 37
 ID AAQ71065 standard; DNA; 20 BP.
 AC AAQ71065;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-APR-1995 (first entry)
 XX
 DE Primer #1 to generate STS 967r for identification of the merlin gene.
 XX
 KM Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;
 KM sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;
 KM neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D2S28;
 KM tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;
 KM merlin-associated tumour; D2S21; posterior capsular lens opacity;
 KM deafness; balance disorder; paralysis; ss.
 XX
 OS Synthetic.
 OS
 PN EP613945-A2.
 XX
 PD 07-SEP-1994.
 XX
 PR 25-FEB-1994; 94BP-00301367.
 PR 25-FEB-1993; 93US-00022034.
 PR 04-MAR-1993; 93US-00026063.
 PR 19-AUG-1993; 93US-00108808.
 PR 22-DEC-1993; 93US-00171718.
 XX
 PA (GEMO) GEN HOSPITAL CORP.
 PI Trofatter JA, Maccollin MM, Gusella JF;
 PI WPI; 1994-272992/34.
 DR
 PT The tumour suppressor gene merlin - for treatment and diagnosis of
 PT tumours and neurofibromatosis (NF2).
 XX
 PS Disclosure; Page 3; 86pp; English.
 PS
 XX The sequences given in AAQ71063-66 are primers which were used in a
 CC sequence-tagged site assay of the region of chromosome 22 surrounding the
 CC NF2 deletions. NF2 is a neurofibromatosis which is characterised by bi-
 CC lateral schwannomas. The NF2 "gene" has been shown by linkage studies to
 CC be assigned to chromosome 22. The missing or mutated gene in NF2 patients
 CC has been shown to be the merlin gene. The gene encodes a protein, merlin
 CC (moesin-erzin-radixin-like protein), which possesses tumour suppressor
 CC activity, and whose tumour suppressor activity is mediated by
 CC interactions with the cytoskeleton. The merlin gene is found on
 CC chromosome 22 between the known markers D2S1 and D2S28. The merlin gene
 CC may be used in gene therapy for the treatment of a merlin-associated
 CC tumour or NF2, or for prevention of schwannoma, meningioma, posterior

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CC capsular lens opacities, deafness or hearing loss, balance disorders or
CC paralysis. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 20 BP; 5 A; 8 C; 1 G; 6 T; 0 U; 0 Other;
Query Match      2.2%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      118 ACATCCTTTTCAC 130
      |||||
      8 ACATCCTTTTCAC 20
RESULT 38
AAV68469
ID AAV68469 standard; DNA; 20 BP.
XX
AC AAV68469;
XX
DT 22-MAR-1999 (first entry)
XX
DE Oligo contained activator-antisense complex spa4-anti-(M3)hTR.
XX
KM Human; telomerase; hTR; activator-antisense complex; malignant; enzyme;
KM cleave; brain; tumour malignant glioma; breast tumour; renal cell cancer;
KM melanoma; prostate cancer; leukemia; polycythemia vera; myeloma; sarcoma;
KM Hodgkin's lymphoma; Waldenstrom's macroglobulinemia; heavy chain disease;
KM carcinoma; chemotherapeutic; antisense; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key      Location/Qualifiers
FT modified_base 1
FT      /*tag= a
FT      /note= "Sp5'A(2'p5'A)3-Bu2"
FT misc_feature 19..20
FT      /*tag= b
FT      /note= "3'-3' internucleotide linkage"
FT misc_feature 20
FT      /*tag= c
FT      /note= "nucleotide in reverse orientation 3'-5'"
XX
PN WO9847911-A1.
XX
PD 29-OCT-1998.
XX
PF 13-APR-1998; 98WO-US007397.
XX
PR 21-APR-1997; 97US-0044507P.
PR 03-FEB-1998; 98US-00018125.
XX
PA (CLEV-) CLEVELAND CLINIC FOUND.
PA (USSH ) US NAT INST OF HEALTH.
XX
PI Silverman RH, Kondo S, Cowell JK, Li G, Torrence PF;
XX
DR WPI; 1998-609972/51.
XX
PT New RNase L activator-telomerase antisense complex - useful to inhibit
PT telomerase activity in telomerase-expressing malignancies.
XX
PS Example; Page 45; 81pp; English.
XX
CC This represents an antisense oligonucleotide to the RNA component of
CC human telomerase (hTR) comprised in the. The invention relates to an
CC activator-antisense complex that comprises: (a) an antisense oligo,
CC complementary to a 12-25 nucleotide portion of the RNA component of hTR,
CC with a hydroxyl moiety at the first end; and (b) a linker attached to the
CC first end; and (c) an activator of RNase L attached to the linker. The
CC activator-antisense complex may be used for inhibiting the growth of a
CC telomerase-expressing malignant cell or tumour. The complex is used to

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CC specifically cleave the ribonucleotide portion of a telomerase enzyme.
CC The complex inhibits growth of telomerase expressing malignant cells from
CC brain tumour malignant glioma, breast tumour, renal cell cancer,
CC melanoma, and prostate cancer. Many other malignancies and related
CC disorders, may be treated including various acute and chronic leukemias,
CC polycythemia vera, Hodgkin's and non-Hodgkin's lymphomas, multiple
CC myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid
CC tumours, including numerous sarcomas and carcinomas. The complex is
CC preferably administered in combination with a chemotherapeutic agent,
CC particularly either cisplatin, doxorubicin, mitomycin, daunorubicin,
CC bleomycin, actinomycin D, or neocarzinostatin. The present sequence is an
CC example of a modified antisense oligo comprised in an activator-antisense
CC complex spa4-anti-(M3)hTR.
XX
SQ Sequence 20 BP; 4 A; 6 C; 7 G; 3 T; 0 U; 0 Other;
Query Match      2.2%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      395 CCGGGGTGCAGAT 407
      |||||
      3 CCGGGGTGCAGAT 15
Db
RESULT 39
AAZ37511/C
ID AAZ37511 standard; DNA; 20 BP.
XX
AC AAZ37511;
XX
DT 07-JAN-2000 (first entry)
XX
DE Human mdm2 phosphorothioate oligodeoxynucleotide #41.
XX
KM Human mdm2 gene; proliferation; tumour; phosphorothioate; p53; cancer;
KM antisense; modulation; oligonucleotide; expression; inhibition;
KM hyperproliferation; blood cancer; brain cancer; breast cancer;
KM lung cancer; soft tissue cancer; psoriasis; fibrosis; atherosclerosis;
KM restenosis; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9949065-A1.
XX
PD 30-SEP-1999.
XX
PF 26-MAR-1999; 99WO-US006702.
XX
PR 26-MAR-1998; 98US-00048810.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX
DR WPI; 1999-610754/52.
XX
PT New antisense compounds used to treat eg. hyperproliferative conditions.
XX
PS Example 9; Page 47; 157pp; English.
XX
CC AAZ37473-Z37738 represent human mdm2 phosphorothioate oligonucleotides.
CC AAZ37471, AAZ37472, AAZ37739, AAZ37740 and AAZ37741 are used in the
CC exemplification of the present invention. The present invention describes
CC novel nucleotide antisense compounds, targeted to the 5' untranslated,
CC translation termination codon, or 3' untranslated region of a nucleic
CC acid encoding human mdm2, that modulates expression of human mdm2. The
CC oligonucleotides mediate their effect by antisense inhibition of
CC hyperproliferative gene expression. The antisense compound is used to
CC treat an animal having a disease or condition associated with mdm2,
CC particularly a hyperproliferative condition, more particularly cancer,
CC especially of the blood, brain, breast, lung or soft tissue, or

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CC peoriastis, fibrosis, atherosclerosis or restenosis

XX Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;

SQ

Query Match 2.2%; Score 13; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 364 GAGCCCGAGGGGC 376

DB 19 GAGCCCGAGGGGC 7

RESULT 40

AAx87306

ID AAX87306 standard; DNA; 20 BP.

AC AAX87306;

DT 27-SEP-1999 (first entry)

DE PRO509 reverse PCR primer 50148.tm.r1.

XX PRO509; cancer; tumour; diagnosis; therapy; human; PCR; primer; ss.

OS Synthetic.

XX Homo sapiens.

XX MO9935170-A2.

PD 15-JUL-1999.

PF 05-JAN-1999; 99WO-US000106.

XX 05-JAN-1998; 98US-0070440P.

PR 29-APR-1998; 98US-0083500P.

PR 22-MAY-1998; 98US-0086414P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-NOV-1998; 98US-0107833P.

PR 20-NOV-1998; 98US-0109304P.

XX (GETH) GENENTECH INC.

XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;

PI Wood WI;

XX WPI; 1999-430385/36.

PT Antibody against proteins expressed in neoplastic cells, useful for tumor

PT diagnosis and treatment.

XX Example 2; Page 55; 162pp; English.

PS This is the nucleotide sequence of reverse primer 50148.tm.r1 that can be

XX used in the PCR amplification of DNA50148 (see AAX87265) nucleic acids

CC coding for PRO509 (see AAY06488). This gene is amplified in various

CC tumour lines. The invention identifies 14 genes (see AAX87254-67) that

CC are amplified in the genome of certain human lung, colon and/or breast

CC cancers and/or cell lines. This gene amplification is expected to be

CC associated with overexpression of the gene product and to contribute to

CC tumorigenesis. The encoded proteins (see AAY06477-90) may be useful

CC targets for the diagnosis and/or treatment of certain cancers, and may

CC act as predictors of the prognosis of tumour treatment

XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;

SQ

Query Match 2.2%; Score 13; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TGGACAGCCTCTT 14

DB 6 TGGACAGCCTCTT 18

RESULT 41

AAA38137/c

ID AAA38137 standard; DNA; 20 BP.

XX AAA38137;

AC 30-AUG-2000 (first entry)

XX Polynucleotide used for ddl gene detection.

XX D alanine:D alanine ligase; ddl, detect; Streptococcus; Enterococcus; ss.

XX Streptococcus sp.

XX US6054269-A.

XX 25-APR-2000.

PF 25-JUN-1997; 97US-00882501.

XX 25-JUN-1997; 97US-00882501.

XX (INSP) INST PASTEUR.

PA Garnier F, Gerbaud G, Dutka-Malen S, Charles M, Evers S;

PI Casadevall B, Gailmond M, Courvalin P;

XX WPI; 2000-338486/29.

XX New polynucleotides derived from unknown sequences internal to the ddl

PT genes coding for D-Alanine:D-Alanine ligase of various bacterial strains

PT belonging to Enterococci or Streptococci genus, useful as probes.

XX Claim 2; Col 57; 42pp; English.

XX Sequences AAA38133-A38148 represent polynucleotides that hybridise with a

CC nucleic acid sequence encoding a D-alanine:D-alanine ligase of a given

CC species belonging to the Streptococci or Enterococci species. The

CC polynucleotides are used to detect bacteria belonging to the Streptococci

CC and Enterococci genus in a sample. The polynucleotides are also used as

CC probes or primers that are specific for particular species or groups of

CC species belonging to Streptococci or Enterococci genus. The

CC oligonucleotide probes are also useful as capture probes immobilized on a

CC substrate to capture a target nucleic acid and can be used in a detection

CC device comprising a matrix library of probes immobilized on a substrate

XX Sequence 20 BP; 8 A; 3 C; 6 G; 3 T; 0 U; 0 Other;

SQ

Query Match 2.2%; Score 13; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 335 GCCTCTACTTCTG 347

DB 15 GCCTCTACTTCTG 3

RESULT 42

AAc60546/c

ID AAc60546 standard; DNA; 20 BP.

AC AAc60546;

XX 31-JAN-2001 (first entry)

DT Human fra-1 mRNA antisense oligonucleotide ISIS 109037.

XX Human fra-1; antisense oligonucleotide; phosphorothioate; cytosatic;

XX antiinflammatory; 2'-methoxyethyl wing; 2'-MOE wing; infection; cancer;

XX ss.

```

OS Homo sapiens.
OS Synthetic.
XX
XX US6124133-A.
XX
XX 26-SEP-2000.
XX
XX 15-OCT-1999; 99US-00418641.
XX
XX 15-OCT-1999; 99US-00418641.
XX
XX 15-OCT-1999; 99US-00418641.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Taylor JK, Cowsett LM;
XX
XX WPI; 2000-601552/57.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to human fra
PT -1 and which specifically hybridizes with and inhibits the expression of
PT human fra-1, useful for modulating the expression of fra-1 in cells.
XX
XX Claim 3; Col 41; 38pp; English.
XX
XX The present sequence is one of a large number of antisense
CC oligonucleotides which are targeted to nucleic acids encoding fra-1. The
CC sequences may be oligodeoxyribonucleotides or chimeric oligonucleotides
CC containing a central gap region consisting of ten 2'-deoxynucleotides,
CC which is flanked on both sides by 2'-methoxyethyl (2'-MOE) wings. The
CC oligonucleotides have a phosphorothioate backbone and the cytidine
CC residues in the 2'-MOE wings are 5-methylcytidines. The fra-1 antisense
CC oligonucleotides are useful for inhibiting the expression of fra-1 in
CC human cells or tissues. They can be used for diagnostics, therapeutics,
CC prophylaxis and as research reagents and in kits. Use of the antisense
CC compounds may also be useful prophylactically, e.g. to prevent or delay
CC infection, inflammation or tumour formation
XX
XX Sequence 20 BP; 1 A; 9 C; 3 G; 7 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 GAACCGAGGAG 30
DB 13 GAACCGAGGAG 1

```

RESULT 43

AAA46974
ID AAA46974 standard; cDNA; 20 BP.

```

XX
XX AAA46974;
XX
XX 03-OCT-2000 (first entry)
XX
XX Probe used to isolate cDNA encoding novel polypeptide PRO509.
XX
XX PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO557; PRO715;
XX PRO1017; PRO1112; PRO509; PRO853; PRO862; tumour cell probe;
XX tumorigenesis; cancer; neoplastic cell growth; cell proliferation;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX WO200037640-A2.
XX
XX 29-JUN-2000.
XX
XX 16-DEC-1999; 99WO-US030095.
XX
XX 22-DEC-1998; 98US-0113296P.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.

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PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028565.
XX
XX (GETH ) GENENTECH INC.
XX
XX Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;
XX Wood WI;
XX WPI; 2000-452188/39.
XX
XX New anti-polypeptide antibody useful in the treatment and diagnosis of
PT neoplastic cell growth and proliferation.
XX
XX Example 17; Page 111; 220pp; English.
XX
XX PCR primers AAA46972-73 and probe AAA46974 were used to isolate cDNA
CC encoding a novel human polypeptide. The specification describes novel
CC polypeptides designated PRO201, PRO292, PRO327, PRO1265, PRO344, PRO343,
CC PRO347, PRO357, PRO715, PRO1017, PRO1112, PRO509, PRO853 and PRO862.
CC These genes are amplified in the genome of tumour cells. The polypeptides
CC are believed to contribute to tumorigenesis. The polypeptides are useful
CC targets for the identification of certain cancers, and may act as
CC predictors of the prognosis of tumour treatment. Antibodies against these
CC polypeptides are useful in the treatment and diagnosis of neoplastic cell
XX growth and proliferation in mammals
XX
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
SQ
Query Match 2.2%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGGACAGCCTCTT 14
DB 6 TGGACAGCCTCTT 18

```

RESULT 44

AAF80665/c
ID AAF80665 standard; DNA; 20 BP.

```

XX
XX AAF80665;
XX
XX 02-MAY-2001 (first entry)
XX
XX Human mdm2 phosphorothioate oligonucleotide #39.
XX
XX Antisense; mdm2; hyperproliferation; cancer; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX US6184212-B1.
XX
XX 06-FEB-2001.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Miraglia LJ, Nero P, Graham MJ, Monia BP, Cowsett LM;
XX WPI; 2001-190948/19.
XX
XX Novel antisense compound 8-30 nucleobases in length targeted to a nucleic
PT acid molecule encoding human mdm-2 useful for modulating the expression
PT of human mdm-2 and reducing hyperproliferation of human cells.

```

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PS Example 9; Col 27; 77bp; English.
XX
CC The present invention relates to an antisense compound 8-30 nucleobases
CC in length targeted to nucleobases 1-308 of the 5' untranslated region,
CC 1776-1806 of the translation termination codon region or 1818-2370 of the
CC 3' untranslated region of a nucleic acid molecule encoding human mdm-2.
CC The invention is useful for reducing hyperproliferation of human cells,
CC modulating the expression of mdm2 in human cells or tissues or in vitro.
CC The hyperproliferative disorder includes cancer or psoriasis
XX
SQ Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.2%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7
XX
RESULT 45
ID AAS29280 standard; DNA; 20 BP.
XX
AC AAS29280;
XX
XX 21-NOV-2001 (first entry)
XX
DE Human mdm2 antisense oligonucleotide 31716.
XX
KW Human; mdm2; hyperproliferative disorder; cancer; psoriasis;
KW atherosclerosis; tumour; cytostatic; anti psoriatic;
KW anti arteriosclerotic; vasotropic; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= All phosphorothioate linkages,
FT additionally bases 1-6 and bases 15-20 are 2'-O-
FT methoxyethyl bases, and bases 7-14 are deoxynucleotides"
XX
XX US2001016575-A1.
XX
XX 23-AUG-2001.
XX
XX 02-JAN-2001; 2001US-00752983.
XX
XX 26-MAR-1998; 98US-00048810.
XX
XX 26-MAR-1999; 99US-00280805.
XX
XX (MIRA/) MIRA/LIA L J.
XX
XX (NERO/) NERO P.
XX
XX (GRAH/) GRAHAM M J.
XX
XX (MONI/) MONIA B P.
XX
XX (COMS/) COMSERT L M.
XX
XX MIRA/LIA L J, NERO P, GRAHAM M J, MONIA B P, COMSERT L M;
XX
XX WPI; 2001-535565/59.
XX
XX An antisense compound, useful for treating e.g. cancer, comprises
XX nucleobases targeted a region (e.g. translation termination codon region)
XX of a nucleic acid encoding human mdm2.
XX
XX Example 9; Page 15; 81bp; English.
XX
XX The present invention relates to antisense compounds, 8-30 nucleobases in
XX length targeted to the 5' untranslated region, translation termination
XX codon region, 3' untranslated region, coding region or translation start

```

```

CC site of a nucleic acid encoding human mdm2, where the antisense compound
CC modulates the expression of human mdm2. The antisense oligonucleotides of
CC the invention are useful for encoding human mdm2 and for inhibiting the
CC expression of human mdm2. They may be used for treating an animal having
CC a disease or condition associated with amplification of mdm2 gene or
CC overexpression of mdm2 e.g. a hyperproliferative disorder such as cancer
CC (blood, brain, breast, lung, or a soft tissue cancer) and psoriasis,
CC fibrosis, atherosclerosis or restenosis, tumours, colorectal carcinoma
CC and chronic myelogenous leukemia. The antisense compound may be
CC administered with a chemotherapeutic agent to overcome drug resistance.
CC The antisense compound reduces hyperproliferation of human cells. The
CC method, which involves the use of the antisense compound, is also useful
CC for detecting the role of mdm2 expression in various cell functions and
CC physiological processes and useful in both clinical research and
CC diagnostic tools. AAS29242-AAS29507 represent the human mdm2 antisense
CC oligonucleotides of the present invention
XX
SQ Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.2%; Score 13; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 364 GAGCCCGAGGGGC 376
Db 19 GAGCCCGAGGGGC 7
XX
RESULT 46
ID AAL42131 standard; DNA; 20 BP.
XX
AC AAL42131;
XX
XX 27-MAY-2002 (first entry)
XX
DE Human KLF6 gene exon 2 PCR primer 2AF3.
XX
XX Human; PCR; primer; ss; Kruppel-like factor 6; KLF6; 2AF3;
XX tumour suppressor gene; cancer risk; prostate cancer; neuroblastoma;
XX glioblastoma; melanoma; breast cancer; ovarian cancer;
XX squamous cell carcinoma; hepatocellular cancer; lung cancer;
XX colon cancer; benign hyperplasia; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200212894-A1.
XX
XX 14-FEB-2002.
XX
XX 09-AUG-2001; 2001WO-US025046.
XX
XX 09-AUG-2000; 2000US-022411P.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Friedman S, Li D, Naria G, Martignetti J, Heath K;
XX
XX WPI; 2002-241784/29.
XX
XX Detecting inactivation or alteration of a Kruppel-like factor 6 (KLF6)
XX gene, useful for diagnosing or determining the relative risk of a cancer
XX (e.g. neuroblastoma or breast cancer) by detecting modifications of the
XX KLF6 genomic DNA.
XX
XX Example 7; Page 63; 103bp; English.
XX
XX The invention comprises a method for detecting a modification in genomic
XX DNA, causing inactivation or alteration of a Kruppel-like factor 6 (KLF6)
XX tumour suppressor gene. The method of the invention is useful for
XX diagnosing, prognosing or determining the relative risk of a cancer (i.e.
XX prostate cancer, neuroblastoma, glioblastoma, melanoma, breast cancer,
XX ovarian cancer, head and neck squamous cell carcinoma, hepatocellular

```

CC cancer, lung cancer, or colon cancer. The method is also useful for
 CC preventing or treating human hyperplasia (e.g. benign hyperplasia), or
 CC cancers. The KLF6 gene sequence is useful for expressing the KLF6 protein
 CC in somatic cell types for human gene therapy. The present sequence
 CC represents a PCR primer specific for the human KLF6 gene sequence
 XX
 SQ Sequence 20 BP; 2 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 539 TTTTGCCCTGTA 551
 |||||
 DB 3 TTTTGCCCTGTA 15

RESULT 47

AL40381
 ID AAL40381 standard; DNA; 20 BP.

XX
 AC AAL40381;

XX 19-SEP-2002 (first entry)

DE Mouse caspase 6 antisense inhibition related oligo SEQ ID No 100.

XX Muscular; cytoskeletal; neurotrophic; neuroprotective; ophthalmological;
 KM antileptemic; osteopathic; caspase 6; Rieger's syndrome; bone metabolism;
 KM ataxia telangiectasia; hyperproliferative disorder; cholesterol disorder;
 KM haematopoietic disorder; cancer; neurological; Alzheimer's disease;
 KM apoptotic; mouse; murine; de.

XX Mus musculus.

PN WO200229066-A1.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US030871.

XX 04-OCT-2000; 2000US-00679299.

XX (ISIS-) ISIS PHARM INC.

PI Brown-Driver VL, Zhang H, Watt AT;

DR WPI; 2002-471315/50.

PT An antisense oligonucleotide of 8 to 50 nucleotides in length that
 PT inhibits caspase 6, is useful for treating Rieger's syndrome.

PS Claim 3; Page 91; 141pp; English.

XX The invention relates to an antisense oligonucleotide compound of 8 to 50
 CC nucleotides in length that is targeted to a nucleic acid molecule
 CC encoding caspase 6, where the oligonucleotide specifically hybridizes
 CC with and inhibits the expression of caspase 6. The oligonucleotide of the
 CC invention specifically hybridizes to and inhibits expression of caspase 6
 CC in cells or tissues. The oligonucleotides can be administered
 CC therapeutically or prophylactically to treat an animal having a disease
 CC or condition associated with caspase 6, such as Rieger's syndrome or
 CC ataxia telangiectasia, hyperproliferative disorder, a haematopoietic
 CC disorder, a bone metabolism or cholesterol disorder, various types of
 CC cancer, neurological conditions such as Alzheimer's disease and other de-
 CC regulated apoptotic pathological conditions. This polynucleotide sequence
 CC represents a mouse caspase 6 oligonucleotide relating to the invention.
 CC NOTE: This phosphorothioate oligonucleotide sequence has 2'-MOB wings and
 CC a deoxy gap

SQ Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 447 TACTTTGTAGAA 459
 |||||
 DB 4 TACTTTGTAGAA 16

RESULT 48

ABK70785/c
 ID ABK70785 standard; DNA; 20 BP.

XX
 AC ABK70785;

DT 15-JUL-2002 (first entry)

DE Human TSPI domain containing gene sequencing primer KY01-518.

XX TSPI; thrombospondin domain; DNA sequencing; primer; ss; FG06969;
 KM FG01896; angiogenesis; vasculogenesis.

XX Homo sapiens.

PN JP2002085059-A.

PD 26-MAR-2002.

XX 08-SEP-2000; 2000JP-00273778.

XX 08-SEP-2000; 2000JP-00273778.

XX (KAZU-) ZH KAZUSA DNA KENKUSHO.

XX (YOSH) YOSHITOMI PHARM IND KK.

DR WPI; 2002-378268/41.

PT TSPI domain-containing polypeptide useful for drug compositions.

PS Example 2; Page 15; 51pp; Japanese.

XX The invention relates to a TSPI (thrombospondin 1) domain-containing
 CC polypeptide comprising the proteins appearing as AA080188 and AA080189,
 CC encoded by cDNAs designated FG06969 and FG01896. Also included are
 CC proteins that are 50% homologous to the proteins and a polypeptide having
 CC at least one deletion, replacement, addition or insertion of amino acid
 CC in the protein and having at least 8 repetitions of the TSPI domain. The
 CC polypeptide can be used in drug compositions particularly for disorders
 CC associated with angiogenesis and vasculogenesis. The present sequence is
 CC a sequencing primer for the cDNAs of the invention

SQ Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.2%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 206 ACCTAGACCTGG 218
 |||||

DB 15 ACCTAGACCTGG 3

RESULT 49

AAL46719/c
 ID AAL46719 standard; DNA; 20 BP.

XX
 AC AAL46719;

DT 20-AUG-2002 (first entry)

DE Human serine-threonine protein kinase coding sequence PCR primer #1.

XX Human; serine-threonine protein kinase; cancer; diabetes; obesity;
 KM central nervous system disorder; inflammation; gene therapy; COPD;

KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
 KW antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
 KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
 KW PCR; enzyme; primer; ss.
 XX Homo sapiens.
 XX PN WO200233056-A2.
 XX PD 25-APR-2002.
 XX PF 15-OCT-2001; 2001WO-EP011892.
 XX PR 16-OCT-2000; 2000US-02400972.
 XX PR 30-JUL-2001; 2001US-0308096P.
 XX PA (FARB) BAYER AG.
 XX PI Koehler RH;
 XX DR WPI; 2002-435534/46.
 XX PT New human serine-threonine protein kinase and encoding polynucleotides,
 PT useful for diagnosing, treating and preventing central nervous system
 PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
 XX PS Example 11; Page 95; 135pp; English.
 XX CC The present invention provides the protein and coding sequences of a
 CC human serine-threonine protein kinase. The sequences can be used in the
 CC diagnosis, treatment and prevention of cancers (e.g. leukemia, lymphoma
 CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
 CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,
 CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
 CC chronic obstructive pulmonary disease (COPD). The present sequence is a
 CC PCR primer for the coding sequence of the invention
 XX SQ Sequence 20 BP; 6 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
 QY Query Match 2.2%; Score 13; DB 6; Length 20;
 Db Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 194 TCTCGACTGGCA 206
 Db 19 TCTCGACTGGCA 7
 RESULT 50
 ID ACC49244
 XX ACC49244 standard; DNA; 20 BP.
 AC ACC49244;
 XX 20-JUN-2003 (first entry)
 DT
 XX Human ribonuclease L antisense oligonucleotide SEQ ID NO:61.
 DE Human ribonuclease L; antisense modulation; cytostatic; antimicrobial;
 KW antiinflammatory; antitumour; ribonuclease L expression inhibitor;
 KW antisense gene therapy; infection; aberrant apoptosis; cancer; tumour;
 KW inflammation; phosphorothioate; 2'-O-methoxyethyl; ss.
 XX Homo sapiens.
 OS Synthetic.
 OS XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkages"
 FT modified_base 1..5
 FT /*tag= b

FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls (2'-MOEs)"
 FT modified_base 15..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-O-methoxyethyls (2'-MOEs)"
 XX PN WO2003023011-A2.
 XX PD 20-MAR-2003.
 XX PF 09-SEP-2002; 2002WO-US028729.
 XX PR 12-SEP-2001; 2001US-00954679.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ward DT, Watt AT;
 XX DR WPI; 2003-313248/30.
 XX PT Novel antisense compound which is targeted to nucleic acid encoding
 PT ribonuclease L, and inhibits expression of ribonuclease L protein, useful
 PT for treating diseases or conditions resulting from infections and
 PT aberrant apoptosis.
 XX PS Claim 3; Page 78; 106pp; English.
 XX CC The present invention describes a compound (I) of 8-50 nucleobases in
 CC length targeted to a nucleic acid molecule (II) encoding ribonuclease L
 CC (III), and which specifically hybridises with (II) and inhibits
 CC expression of (III), where (I) specifically hybridises with at least an 8
 CC nucleobase portion of an active site on (II). (I) has cytostatic,
 CC antitumoral, antiinflammatory and antitumour activities, and can be
 CC used as a ribonuclease L expression inhibitor and in antisense gene
 CC therapy. (I) is useful for inhibiting the expression of ribonuclease L in
 CC cells or tissues, and for treating an animal having a disease condition
 CC associated with ribonuclease L, e.g. infection, aberrant apoptosis or
 CC cancer. (I) is also useful for modulating the process of RNA-mediated
 CC interference (RNAi) in a cell or animal. (I) is also useful
 CC prophylactically, e.g. to prevent or delay infection, inflammation or
 CC tumour formation. (I) is useful as a tool in differential and/or
 CC combinatorial analyses to elucidate expression patterns of a portion or
 CC the entire complement of genes expressed within cells and tissues. (I) is
 CC also useful for research, therapeutics and diagnostics. (I) is also
 CC useful for distinguishing functions of various members of a biological
 CC pathway, and in antisense gene therapy. The present sequence represents a
 CC human ribonuclease L chimeric phosphorothioate antisense oligonucleotide,
 CC which is used in an example from the present invention
 XX SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
 QY Query Match 2.2%; Score 13; DB 7; Length 20;
 Db Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 313 AGCTGAGGATCT 325
 Db 1 AGCTGAGGATCT 13
 RESULT 51
 ID AAD53632/c
 XX AAD53632 standard; DNA; 20 BP.
 AC AAD53632;
 XX 28-MAY-2003 (first entry)
 DT Human PTPN2 antisense oligonucleotide, ISIS #135690.
 XX Human PTPN2 antisense oligonucleotide, ISIS #135690.
 DE Antisense; human; protein tyrosine phosphatase non-receptor type 2;
 KW PTPN2; autoimmune disorder; hyperproliferative condition; cancer;

[illegible]

KW	library screening; Southern hybridisation; northern hybridisation;
KV	dot-blot hybridisation; gene sequence; mutation detection;
KM	target sequence; probe; PCR; primer; ss.
XX	
OS	unidentified.
XX	
PN	US2003082596-A1.
XX	
PD	01-MAY-2003.
XX	
PX	08-AUG-2002; 2002US-00215112.
PR	08-AUG-2001; 2001US-0311040P.
PA	(MITT/) MITTMANN M.
XX	
PI	Mittmann M;
DR	WPI; 2003-576608/54.
XX	
PT	New probe array useful e.g. for monitoring gene expression levels, for
FT	analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT	comprises multiple nucleic acid probes.
XX	
PS	Claim 1; SEQ ID NO 9359; 9pp; English.
XX	
CC	The present invention relates to nucleic acid sequences that are
CC	complementary to particular genes, and can be used as probes for a
CC	variety of analyses such as gene expression analysis. Each probe
CC	comprises 9 or more consecutive nucleotides from at least one of 14936
CC	nucleotide sequences defined in the patent, or their perfect sense match,
CC	sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC	The probes may be used in an array comprising at least 10 distinct
CC	nucleic acid probes. The array is useful in monitoring gene expression
CC	levels by hybridisation to a DNA library, in analysing genetic
CC	variations, and in hybridising tag-labelled compounds. The probes are
CC	useful for identifying family members of a gene. The probes are also
CC	useful in situ hybridisations, in screening cDNA or genomic libraries
CC	(or derived subclones) for additional clones containing segments of DNA
CC	that have been previously isolated and sequenced, in Southern, northern,
CC	or dot-blot hybridisation of genomic DNA to identify or detect the
CC	sequence of any gene or detect specific mutations in any gene, and in
CC	mapping the 5' termini of mRNA molecules by primer extensions. The
CC	nucleic acid sequences of the invention are also useful as PCR primers.
CC	The invention provides a large collection of nucleic acid sequences
CC	complementary to particular genes with a wide range of analytical uses.
CC	ACH50865-ACH55260 represent the target sequences of the invention. Note:
CC	The sequence data for this patent was obtained in electronic format
CC	directly from the USPTO web site at seqdata.uspto.gov/patident.htm1
XX	
SQ	Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
	Query March 2 2%; Score 13; DB 8; Length 20;
	Best Local Similarity 100.0%; Pred. No. 3.8e+04;
	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY	77 AGACCTACTGCTGTG 89
Dd	15 AGACCTACTGCTGTG 3
RESULT 53	
ID	ACH60616
XX	ACH60616 standard; DNA; 20 BP.
AC	ACH60616;
DT	17-OCT-2003 (first entry)
XX	
XX	DNA target sequence #9752 useful in array for genetic analyses.
DE	
XX	Gene expression analysis; array; hybridisation; genetic variation;
KW	tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 OS Unidentified.
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 PI Miltmann M;
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 9752; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdIdentify.html
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 77 AGACCTACTCTGTG 89
 6 AGACCTACTCTGTG 18
 XX
 AC ACH60951;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE DNA target sequence #10087 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KW target sequence; probe; PCR; primer; ss.
 OS Unidentified.
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 PI Miltmann M;
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 10087; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labelled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' termini of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdIdentify.html
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 77 AGACCTACTCTGTG 89
 6 AGACCTACTCTGTG 18
 XX
 AC ACH60952;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE DNA target sequence #10088 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KM target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mitmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 10088; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labeled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdidentry.html
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 3.8e-04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 77 AGACCTACTCTGTG 89
 |||||
 6 AGACCTACTCTGTG 18
 |||||
 RESULT 56
 ACH60727
 ID ACH60727 standard; DNA; 20 BP.
 XX
 AC ACH60727;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE DNA target sequence #9863 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

KW library screening; Southern hybridisation; northern hybridisation;
 KW dot-blot hybridisation; gene sequence; mutation detection;
 KM target sequence; probe; PCR; primer; ss.
 XX
 OS Unidentified.
 PN US2003082596-A1.
 XX
 PD 01-MAY-2003.
 XX
 PF 08-AUG-2002; 2002US-00215112.
 XX
 PR 08-AUG-2001; 2001US-0311040P.
 XX
 PA (MITT/) MITTMANN M.
 XX
 PI Mitmann M;
 XX
 DR WPI; 2003-576608/54.
 XX
 PT New probe array useful e.g. for monitoring gene expression levels, for
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
 PT comprises multiple nucleic acid probes.
 XX
 PS Claim 1; SEQ ID NO 9863; 9pp; English.
 XX
 CC The present invention relates to nucleic acid sequences that are
 CC complementary to particular genes, and can be used as probes for a
 CC variety of analyses such as gene expression analysis. Each probe
 CC comprises 9 or more consecutive nucleotides from at least one of 14936
 CC nucleotide sequences defined in the patent, or their perfect sense match,
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
 CC The probes may be used in an array comprising at least 10 distinct
 CC nucleic acid probes. The array is useful in monitoring gene expression
 CC levels by hybridisation to a DNA library, in analysing genetic
 CC variations, and in hybridising tag-labeled compounds. The probes are
 CC useful for identifying family members of a gene. The probes are also
 CC useful in situ hybridisations, in screening cDNA or genomic libraries
 CC (or derived subclones) for additional clones containing segments of DNA
 CC that have been previously isolated and sequenced, in Southern, northern,
 CC or dot-blot hybridisation of genomic DNA to identify or detect the
 CC sequence of any gene or detect specific mutations in any gene, and in
 CC mapping the 5' terminus of mRNA molecules by primer extensions. The
 CC nucleic acid sequences of the invention are also useful as PCR primers.
 CC The invention provides a large collection of nucleic acid sequences
 CC complementary to particular genes with a wide range of analytical uses.
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
 CC The sequence data for this patent was obtained in electronic format
 CC directly from the USPTO web site at seqdata.uspto.gov/psipdidentry.html
 XX
 SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 QY Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 3.8e-04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 77 AGACCTACTCTGTG 89
 |||||
 6 AGACCTACTCTGTG 18
 |||||
 RESULT 57
 ACH60447/c
 ID ACH60447 standard; DNA; 20 BP.
 XX
 AC ACH60447;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE DNA target sequence #9583 useful in array for genetic analyses.
 XX
 KW Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

```

KM library screening; Southern hybridisation; northern hybridisation;
KM dot-blot hybridisation; gene sequence; mutation detection;
KM target sequence; probe; PCR; primer; ss.
XX
XX
XX OS unidentified.
XX
XX PN US2003082596-A1.
XX
XX PD 01-MAY-2003.
XX
XX PF 08-AUG-2002; 2002US-00215112.
XX
XX PR 08-AUG-2001; 2001US-0311040P.
XX
XX PA (MITT/) MITTMANN M.
XX
XX PI Miltmann M;
XX
XX DR WPI; 2003-576608/54.
XX
XX DR
XX PT New probe array useful e.g. for monitoring gene expression levels, for
XX analyzing genetic variations, or for hybridizing tag-labeled compounds,
XX PT comprises multiple nucleic acid probes.
XX
XX PS Claim 1; SEQ ID NO 9583; 9pp; English.
XX
XX CC The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX CC nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labeled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' terminus of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences
XX complementary to particular genes with a wide range of analytical uses.
XX CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
XX The sequence data for this patent was obtained in electronic format
XX directly from the USPTO web site at seqdata.uspto.gov/psipdsidentry.html
XX
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.2%; Score 13; DB 8; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 77 AGACCTACTGTG 89
XX |||||
XX 15 AGACCTACTGTG 3
XX
XX Db
XX
XX RESULT 58
XX ACH60448/c
XX ID ACH60448 standard; DNA; 20 BP.
XX
XX AC ACH60448;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE DNA target sequence #9584 useful in array for genetic analyses.
XX
XX KM Gene expression analysis; array; hybridisation; genetic variation;
XX tag-labelled compound; gene family; in situ hybridisation;

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```

KM library screening; Southern hybridisation; northern hybridisation;
KM dot-blot hybridisation; gene sequence; mutation detection;
KM target sequence; probe; PCR; primer; ss.
XX
XX
XX OS unidentified.
XX
XX PN US2003082596-A1.
XX
XX PD 01-MAY-2003.
XX
XX PF 08-AUG-2002; 2002US-00215112.
XX
XX PR 08-AUG-2001; 2001US-0311040P.
XX
XX PA (MITT/) MITTMANN M.
XX
XX PI Miltmann M;
XX
XX DR WPI; 2003-576608/54.
XX
XX DR
XX PT New probe array useful e.g. for monitoring gene expression levels, for
XX analyzing genetic variations, or for hybridizing tag-labeled compounds,
XX PT comprises multiple nucleic acid probes.
XX
XX PS Claim 1; SEQ ID NO 9584; 9pp; English.
XX
XX CC The present invention relates to nucleic acid sequences that are
XX complementary to particular genes, and can be used as probes for a
XX variety of analyses such as gene expression analysis. Each probe
XX comprises 9 or more consecutive nucleotides from at least one of 14936
XX nucleotide sequences defined in the patent, or their perfect sense match,
XX sense mismatch, antisense match or antisense mismatch oligonucleotides.
XX The probes may be used in an array comprising at least 10 distinct
XX CC nucleic acid probes. The array is useful in monitoring gene expression
XX levels by hybridisation to a DNA library, in analysing genetic
XX variations, and in hybridising tag-labeled compounds. The probes are
XX useful for identifying family members of a gene. The probes are also
XX useful in situ hybridisations, in screening cDNA or genomic libraries
XX (or derived subclones) for additional clones containing segments of DNA
XX that have been previously isolated and sequenced, in Southern, northern,
XX or dot-blot hybridisation of genomic DNA to identify or detect the
XX sequence of any gene or detect specific mutations in any gene, and in
XX mapping the 5' terminus of mRNA molecules by primer extensions. The
XX nucleic acid sequences of the invention are also useful as PCR primers.
XX The invention provides a large collection of nucleic acid sequences
XX complementary to particular genes with a wide range of analytical uses.
XX CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
XX The sequence data for this patent was obtained in electronic format
XX directly from the USPTO web site at seqdata.uspto.gov/psipdsidentry.html
XX
XX SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.2%; Score 13; DB 8; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.8e-04;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX OY 77 AGACCTACTGTG 89
XX |||||
XX 15 AGACCTACTGTG 3
XX
XX Db
XX
XX RESULT 59
XX ACH60451/c
XX ID ACH60451 standard; DNA; 20 BP.
XX
XX AC ACH60451;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE DNA target sequence #9587 useful in array for genetic analyses.
XX
XX KM Gene expression analysis; array; hybridisation; genetic variation;
XX tag-labelled compound; gene family; in situ hybridisation;

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KM library screening; Southern hybridisation; northern hybridisation;
KM dot-blot hybridisation; gene sequence; mutation detection;
KM target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
FN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mitmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 9587; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patid/patidentry.html
XX
SQ Sequence 20 BP; 6 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

```

Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 77 AGACCTACTCTGTG 89
DB 15 AGACCTACTCTGTG 3

```

RESULT 60
 ACH60955
 ID ACH60955 standard; DNA; 20 BP.
 AC ACH60955;
 DT 17-OCT-2003 (first entry)
 XX
 XX DNA target sequence #10091 useful in array for genetic analyses.
 DE
 XX
 XX Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

```

KM library screening; Southern hybridisation; northern hybridisation;
KM dot-blot hybridisation; gene sequence; mutation detection;
KM target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
FN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
XX
PA (MITT/) MITTMANN M.
XX
PI Mitmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 10091; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/patid/patidentry.html
XX
SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

```

Query Match 2.2%; Score 13; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.8e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 77 AGACCTACTCTGTG 89
DB 6 AGACCTACTCTGTG 18

```

RESULT 61
 ACH60111/c
 ID ACH60111 standard; DNA; 20 BP.
 AC ACH60111;
 DT 17-OCT-2003 (first entry)
 XX
 XX DNA target sequence #9247 useful in array for genetic analyses.
 DE
 XX
 XX Gene expression analysis; array; hybridisation; genetic variation;
 KW tag-labelled compound; gene family; in situ hybridisation;

XX	athleroscclerosis, restenosis, apoptosis modulation; p21; ss;
KM	2'-methoxyethoxy-residue; phosphorothioate backbone.
XX	
OS	Homo sapiens.
XX	
PN	WO2003048315-A2.
XX	
PD	12-JUN-2003.
XX	
PF	02-DEC-2002; 2002WO-US038281.
XX	
PR	04-DEC-2001; 2001US-00005344.
XX	
PA	(ISIS-) ISIS PHARM INC.
XX	
P1	Mitaglia LJ, Nero PS, Graham MJ, Monia BP, Koller E, Chiang MY,
P1	Manoharan M;
XX	
DR	WPI; 2003-577263/54.
XX	
PT	Novel antisense compound targeted to 5' untranslated region, coding
PT	region, or intron-exon junction of nucleic acid molecule encoding mdm2,
PT	useful for treating e.g. cancer, psoriasis or restenosis by inhibiting
PT	mdm2 expression.
XX	
PS	Example 9; SEQ ID NO 41; 289bp; English.
XX	
CC	The invention comprises antisense oligonucleotides which are targeted to
CC	the human mdm2 gene. The antisense oligonucleotides of the invention are
CC	useful for reducing hyperproliferation of human cells. The antisense
CC	oligonucleotides are also useful for treating: hyperproliferative
CC	disorders (e.g. cancer), psoriasis, fibrosis, atherosclerosis, or
CC	restenosis. The antisense oligonucleotides are also useful for modulating
CC	apoptosis, and for increasing expression of p21. The present DNA sequence
CC	represents a human mdm2 gene antisense oligonucleotide of the invention.
CC	The present sequence contains 2'-methoxyethoxy-residues and has a
CC	phosphorothioate backbone.
XX	
SQ	Sequence 20 BP; 0 A; 10 C; 8 G; 2 T; 0 U; 0 Other;
XX	
Query Match	2.2%; Score 13; DB 9; Length 20;
Best Local Similarity	100.0%; Fred.No. 3.6e+04;
Matches 13; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	364 GAGCCCGAGGGGC 376
DB	19 GAGCCCGAGGGGC 7
RESULT 63	
AB134852/c	
ID	AB134852 standard; DNA; 12 BP.
XX	
AC	AB134852;
XX	
DT	22-FEB-2002 (first entry)
XX	
DE	Oligonucleotide primer SEQ ID NO 334825 for detecting SNP TSC0038427.
XX	
KM	SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM	peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM	central nervous system; gastrointestinal; respiratory; immune; metabolic
XX	
OS	Homo sapiens.
XX	
PN	WO200177384-A2.
XX	
PD	18-OCT-2001.
XX	
PF	06-APR-2001; 2001WO-IB000713.
XX	
PR	07-APR-2000; 2000DE-01019173.
XX	

PA (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 334825; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 12 BP; 7 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
 QY
 Query Match 2.0%; Score 12; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 425 AAGATTATTTT 436
 12 AAGATTATTTT 1
 RESULT 64
 AB135151
 ID AB135151 standard; DNA; 12 BP.
 AC AB135151;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 335124 for detecting SNP TSC0038615.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 335124; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic

CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 12 BP; 5 A; 0 C; 1 G; 6 T; 0 U; 0 Other;
 QY
 Query Match 2.0%; Score 12; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 424 AAGATTATTTT 435
 1 AAGATTATTTT 12
 RESULT 65
 AB160311
 ID AB160311 standard; DNA; 12 BP.
 AC AB160311;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide primer SEQ ID NO 360284 for detecting SNP TSC0052014.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 PA (EPiG-) EPIGENOMICS AG.
 PI Olek A, Piepenbrock C, Berlin K;
 PI WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 360284; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 12 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATTATTTT 437
 DB 1 AGATTATTTT 12

RESULT 66
 ABH96686/c
 ID ABH96686 standard; DNA; 12 BP.

AC ABH96686;

DT 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 296679 for detecting SNP TSC0017210.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 296679; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -AB099989, ABP00010-ABP99989, ABH00010-ABH99989 and AB100010-AB182073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

XX AB178279;
 XX 22-FEB-2002 (first entry)

DE Oligonucleotide primer SEQ ID NO 378252 for detecting SNP TSC0062690.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.

XX WO200177384-A2.

XX 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is

XX designed to detect single-nucleotide polymorphisms and cytosine

XX methylation status.

XX Claim 1; SEQ ID NO 378252; 29pp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic

XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)

XX and cytosine methylation status in chemically pretreated genomic DNA. The

XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a

XX range of diseases including immune system, gastrointestinal, respiratory,

XX central nervous system, cardiovascular and metabolic disorders. The

XX oligomers are also used for detecting cell type differentiation. ABC00010

XX -AB099989, ABP00010-ABP99989, ABH00010-ABH99989 and AB100010-AB182073

XX represent the oligomers described in the invention. NOTE: The sequence

XX data for this patent did not form part of the printed specification, but

XX was obtained in electronic format from WIPO at

XX ftp.wipo.int/pub/published_pct_sequences

Query Match 2.0%; Score 12; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 436
 DB 1 AAGATTATTTT 12

RESULT 68
 ABC01330
 ID ABC01330 standard; DNA; 13 BP.

AC ABC01330;

DT 20-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 1321 for detecting SNP TSC0000450.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;

KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;

XX central nervous system; gastrointestinal; respiratory; immune; metabolic.

OS Homo sapiens.


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PN WO200177384-A2.
XX
XX 18-OCT-2001.
PD
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
PT
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 1321; 29bp + Sequence listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, cardiovascular, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABH00010-ABF99989, ABH00010-ABH99989 and ABH00010-ABI182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ
SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other;
XX
Query March 2, 0%; Score 12; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 426 AGATTATTTTAA 437
Db 1 AGATTATTTTAA 12
| | | | | | | |
RESULT 69
AC ABC54252/c
XX ABC54252 standard; DNA; 13 BP.
XX
DT 21-FEB-2002 (first entry)
DE Oligonucleotide SEQ ID NO 54269 for detecting SNP TSC0014903.
XX
XX SNF; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX
XX WO200177384-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-IB000713.
XX
XX 07-APR-2000; 2000DE-01019173.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2001-657177/75.
XX
```

XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 54269; 29pp + Sequence Listing; German.
 PS
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ASC00010
 CC -ABG9989, ABH00010-ABG9989, ABH00010-ABH9989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 8 A; 0 C; 1 G; 4 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. NO. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 QY 428 ATTAATTTTACT 439
 DB |||||
 12 ATTAATTTTACT 1
 RESULT 70
 ID ABRF95377
 XX ABRF95377 standard; DNA; 13 BP.
 AC ABRF95377;
 XX
 XX 22-FEB-2002 (first entry)
 DT
 XX
 DE Oligonucleotide SEQ ID NO 195374 for detecting SNP TSC0048069.
 XX
 KW SN; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX
 XX WO200177384-A2.
 PN
 XX
 PD 18-OCT-2001.
 PD
 XX
 PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS
 XX Claim 1; SEQ ID NO 195374; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC

CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC

XX Sequence 13 BP; 3 A; 2 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTTACT 439
 DB 2 ATTATTTTACT 13

RESULT 71
 ABF99192
 ID ABF99192 standard; DNA; 13 BP.
 XX
 AC ABF99192;
 XX
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 199189 for detecting SNP TSC0049016.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX

OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX

PS Claim 1; SEQ ID NO 199189; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC

XX Sequence 13 BP; 4 A; 0 C; 1 G; 7 T; 0 U; 1 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 426 AGATATTTTAA 437
 DB 1 AGATATTTTAA 12

RESULT 72
 ABH06778/c
 ID ABH06778 standard; DNA; 13 BP.
 XX
 AC ABH06778;
 XX
 DT 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 206755 for detecting SNP TSC0050584.

XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX

OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.

PR 07-APR-2000; 2000DE-01019173.

PA (EPIC-) EPIGENOMICS AG.

PI Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-657177/75.

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX

PS Claim 1; SEQ ID NO 206755; 29pp + Sequence listing; German.

CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC

XX Sequence 13 BP; 3 A; 0 C; 2 G; 7 T; 0 U; 1 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CAATCAAAAT 51
 DB 12 CAATCAAAAT 1

RESULT 73
 ABH06779
 ID ABH06779 standard; DNA; 13 BP.
 XX
 AC ABH06779;
 XX
 DT 22-FEB-2002 (first entry)

XX

DE Oligonucleotide SEQ ID NO 206756 for detecting SNP TSC0050584.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 206756; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 13 BP; 7 A; 2 C; 0 G; 3 T; 0 U; 1 Other;
 SQ
 XX
 XX Query Match 2.0%; Score 12; DB 5; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPiG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PS Claim 1; SEQ ID NO 195373; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 CC Sequence 13 BP; 8 A; 0 C; 2 G; 3 T; 0 U; 0 Other;
 SQ
 XX
 XX Query Match 2.0%; Score 12; DB 5; Length 13;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ATTATTTTACT 439
 DB 12 ATTATTTTACT 1

RESULT 75
 ABF8871/c
 ID ABF88871 standard; DNA; 13 BP.
 AC ABF88871;
 XX 22-FEB-2002 (first entry)
 DE Oligonucleotide SEQ ID NO 18868 for detecting SNP TSC0046496.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 PD 06-APR-2001; 2001WO-IB000713.
 XX 07-APR-2000; 2000DE-01019173.
 XX (EPiG-) EPIGENOMICS AG.
 PA Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 DR Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.

PS Claim 1; SEQ ID NO 18868; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 425 AAGATTATTTT 436
DB 13 AAGATTATTTT 2
RESULT 76
ABF35048/c
ID ABF35048 standard; DNA; 13 BP.
XX
AC ABF35048;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 135045 for detecting SNP TSC0033667.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX MPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 135045; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 4 A; 0 C; 2 G; 7 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 CAATCAAAAT 51
DB 12 CAATCAAAAT 1
RESULT 77
ABF51823/c
ID ABF51823 standard; DNA; 13 BP.
XX
AC ABF51823;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 151820 for detecting SNP TSC0038356.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIC-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
XX MPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 151820; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABG9989, ABF00010-ABF9989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 5 A; 2 C; 0 G; 6 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 450 TTTTGTAGAAA 461
DB 12 TTTTGTAGAAA 1

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RESULT 78
ABC01331/c
ID ABC01331 standard; DNA; 13 BP.
XX
AC ABC01331;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 1322 for detecting SNP TSC0000450.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 1322; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 8 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 426 AGATTATTTTA 437
DB 13 AGATTATTTTA 2
XX
RESULT 79
ABF13246/c
ID ABF13246 standard; DNA; 13 BP.
XX
AC ABF13246;
XX
DT 21-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 113243 for detecting SNP TSC0028347.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX

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XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2001-657177/75.
XX
PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX
PS Claim 1; SEQ ID NO 113243; 29pp + Sequence Listing; German.
XX
CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 13 BP; 3 A; 1 C; 7 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 182 TCTCCGCGCTACA 193
DB 13 TCTCCGCGCTACA 2
XX
RESULT 80
ABC22482/c
ID ABC22482 standard; DNA; 13 BP.
XX
AC ABC22482;
XX
DT 20-FEB-2002 (first entry)
XX
DE Oligonucleotide SEQ ID NO 22499 for detecting SNP TSC0004446.
XX
KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
OS Homo sapiens.
XX
PN WO200177384-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-IB000713.
XX
PR 07-APR-2000; 2000DE-01019173.
XX
PA (EPIG-) EPIGENOMICS AG.
XX

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PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 22499; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 1 A; 0 C; 8 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 301 AACCCCAACCTC 312
 13 AACCCCAACCTC 2
 XX
 RESULT 81
 ABC54253
 ID ABC54253 standard; DNA; 13 BP.
 XX
 AC ABC54253;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 54270 for detecting SNP TSC0014903.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WC200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001MO-IB000713.
 XX
 PR 07-APR-2000; 2000DB-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 54270; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The

CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 1 C; 0 G; 8 T; 0 U; 0 Other;
 XX
 QY Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Db 428 ATTATTTTACT 439
 2 ATTATTTTACT 13
 XX
 RESULT 82
 ABC75762/C
 ID ABC75762 standard; DNA; 13 BP.
 XX
 AC ABC75762;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 75779 for detecting SNP TSC0019426.
 XX
 KM SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WC200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001MO-IB000713.
 XX
 PR 07-APR-2000; 2000DB-01019173.
 XX
 PA (EPIC-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 75779; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and ABI00010-ABI82073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 2 A; 0 C; 3 G; 8 T; 0 U; 0 Other;
 XX
 QY Query Match 2.0%; Score 12; DB 5; Length 13;

PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 PR 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPiG-) EPIGENOMICS AG.
 PA
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 XX Claim 1; SEQ ID NO 199190; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 7 A; 1 C; 0 G; 4 T; 0 U; 1 Other;
 XX
 Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 426 AGATTATTTT 437
 DB 13 AGATTATTTT 2
 XX
 RESULT 86
 ABC22483
 ID ABC22483 standard; DNA; 13 BP.
 XX
 AC ABC22483;
 XX
 DT 20-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 22500 for detecting SNP TSC0004446.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPiG-) EPIGENOMICS AG.
 PA
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is

PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 22500; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 13 BP; 4 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 301 AACCCCAACTC 312
 DB 1 AACCCCAACTC 12
 XX
 RESULT 87
 ABF51822
 ID ABF51822 standard; DNA; 13 BP.
 XX
 AC ABF51822;
 XX
 DT 21-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 151819 for detecting SNP TSC0038356.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 XX 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 XX
 XX (EPiG-) EPIGENOMICS AG.
 PA
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX WPI; 2001-657177/75.
 DR
 XX
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 XX
 PS Claim 1; SEQ ID NO 151819; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073

CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 13 BP; 6 A; 0 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 450 TTTTGTAGAAA 461
 DB 2 TTTGTAGAAA 13

RESULT 88
 ABF88870
 ID ABF88870 standard; DNA; 13 BP.
 AC ABF88870;
 XX
 XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 188867 for detecting SNP TSC0046496.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
 OS
 XX
 XX WO200177384-A2.
 PN
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIC-) EPIDENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX
 PS Claim 1; SEQ ID NO 188867; 29bp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 13 BP; 4 A; 0 C; 1 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 425 AAGATTATTTT 436
 |||||||

DB 1 AAGATTATTTT 12

RESULT 89
 ABH62102/c
 ID ABH62102 standard; DNA; 13 BP.
 AC ABH62102;
 XX
 XX 22-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 262079 for detecting SNP TSC0063588.
 XX
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KM peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KM central nervous system; gastrointestinal; respiratory; immune; metabolic.

XX Homo sapiens.
 OS
 XX
 XX WO200177384-A2.
 PN
 PD 18-OCT-2001.

PF 06-APR-2001; 2001WO-IB000713.
 XX
 XX 07-APR-2000; 2000DE-01019173.
 PR
 XX (EPIC-) EPIDENOMICS AG.
 PA
 XX Olek A, Piepenbrock C, Berlin K;
 PI
 XX WPI; 2001-657177/75.
 DR

PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single-nucleotide polymorphisms and cytosine
 PT methylation status.
 PT
 XX
 PS Claim 1; SEQ ID NO 262079; 29bp + Sequence Listing; German.

XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation. ABC00010
 CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and AB100010-AB182073
 CC represent the oligomers described in the invention. NOTE: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 13 BP; 1 A; 0 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 AACCCCAACCTC 312
 DB 12 AACCCCAACCTC 1

RESULT 90
 ABF35049
 ID ABF35049 standard; DNA; 13 BP.
 AC ABF35049;
 XX
 XX 21-FEB-2002 (first entry)

DE Oligonucleotide SEQ ID NO 135046 for detecting SNP TSC0033667.
 XX

KM SNP, single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-1B000713.
XX PR 07-APR-2000; 2000DE-01019173.
XX PA (EPig-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 135046; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 7 A; 2 C; 0 G; 4 T; 0 U; 0 Other;
XX Query Match 2.0%; Score 12; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 40 CAATTCAAAAT 51
DB 2 CAATTCAAAAT 13
RESULT 91
ABH62103
ID ABH62103 standard; DNA; 13 BP.
XX AC ABH62103;
XX DT 22-FEB-2002 (first entry)
XX Oligonucleotide SEQ ID NO 262080 for detecting SNP TSC0063588.
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX OS Homo sapiens.
XX WO200177384-A2.
XX PD 18-OCT-2001.
XX PF 06-APR-2001; 2001WO-1B000713.
XX PR 07-APR-2000; 2000DE-01019173.

XX (EPig-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX DR WPI; 2001-657177/75.
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
PT designed to detect single-nucleotide polymorphisms and cytosine
PT methylation status.
XX PS Claim 1; SEQ ID NO 262080; 29pp + Sequence Listing; German.
XX CC This invention describes novel oligonucleotide primers or peptide nucleic
CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
CC and cytosine methylation status in chemically pretreated genomic DNA. The
CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
CC range of diseases including immune system, gastrointestinal, respiratory,
CC central nervous system, cardiovascular and metabolic disorders. The
CC oligomers are also used for detecting cell type differentiation. ABC00010
CC -ABC99989, ABF00010-ABF99989, ABH00010-ABH9989 and AB100010-AB182073
CC represent the oligomers described in the invention. NOTE: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 13 BP; 5 A; 7 C; 0 G; 1 T; 0 U; 0 Other;
XX Query Match 2.0%; Score 12; DB 5; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 301 AACCCCAACCTC 312
DB 2 AACCCCAACCTC 13
RESULT 92
AAD24072/c
ID AAD24072 standard; DNA; 13 BP.
XX AC AAD24072;
XX DT 09-APR-2002 (first entry)
XX Arabidopsis thaliana KYS transcription factor binding site.
KW Gene expression; maize; ubiquitin promoter; Ubi-1; HSE;
KW heat shock element; agronomic gene; HYS transcription factor; ds.
XX OS Arabidopsis thaliana.
XX WO200194394-A2.
XX PD 13-DEC-2001.
XX PF 08-JUN-2001; 2001WO-US018689.
XX PR 09-JUN-2000; 2000US-00590558.
XX (PROD-) PRODIGENE INC.
XX Jilka JM, Hood BE, Howard JA;
XX WPI; 2002-122117/16.
XX New promoter sequences for causing expression of a structural gene
XX especially agronomic gene or open reading frame in a plant cell,
XX comprises engineered versions of the maize ubiquitin promoter.
XX Disclosure; Page 30; 68pp; English.
XX The invention relates to a promoter sequence capable of directing

CC expression of a nucleotide sequence in a plant cell, comprising maize
 CC ubiquitin (ubi-1) promoter sequence with a modification so that it does
 CC not include two overlapping heat shock elements (HSE) or its directs
 CC expression to increase the endosperm/embryo expression ratio of the
 CC protein when compared to the ratio from a wild-type ubiquitin promoter.
 CC The modified ubi-1 promoter comprises a deletion of 3', 5' or both HSEs,
 CC two non-overlapping/adjacent HSEs, replacement of HSEs with a trimer of a
 CC seed specific element from the promoter of pea lectin gene Pe1, or
 CC insertion of a transcription factor binding site in the HSE region. An
 CC expression construct comprising modified ubi-1 promoter is useful for
 CC causing expression of a structural gene (agronomic genes) or open reading
 CC frame in a plant cell. The modified ubi-1 promoter increases expression
 CC levels beyond those observed with native ubiquitin promoter. The present
 CC sequence is Arabidopsis thaliana HYS transcription factor binding site of
 CC Ribulose-1,5-bisphosphate carboxylase gene, used in the present invention
 SQ Sequence 13 BP; 2 A; 5 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 163 TGCCACGTGGA 174
 Db 13 TGCCACGTGGA 2

RESULT 93
 AAT79478/c
 ID AAT79478 standard; DNA; 14 BP.
 AC AAT79478;
 XX
 DT 22-OCT-1997 (first entry)
 DE DNA ligand for adenosine or adenosine 5'-phosphate.
 XX
 DE Adenosine; adenosine-5'-phosphate; adenosine triphosphate; ATP; binding;
 KM ligand; purification; reagent; isolation; determination;
 KM subcellular localisation; catalytic; assay; SELEX;
 KM Systematic Evolution of Ligands by Exponential enrichment; se.
 XX
 OS Synthetic.
 XX
 PN US5631146-A.
 XX
 PD 20-MAY-1997.
 XX
 PF 19-JAN-1995; 95US-00375116.
 XX
 PR 19-JAN-1995; 95US-00375116.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Szostak JM, Huizenga DE;
 XX
 DR WPI; 1997-288574/26.
 XX
 PT Single stranded DNA molecule, which binds adenosine or adenosine-5'-
 PT phosphate - useful as purification reagent, or for determination of
 PT adenosine triphosphate subcellular localisation in vivo.
 XX
 PS Claim 3; Col 63-64; 55pp; English.

CC The present sequence is an adenosine or adenosine-5'-phosphate (ASP)
 CC binding single stranded DNA molecule, which can be used as a purification
 CC reagent for the isolation of adenosine or an ASP, or to determine the
 CC subcellular localisation of, e.g. adenosine triphosphate (ATP), in vivo.
 CC The DNA molecule was prepared by contacting DNA molecules having a region
 CC of random sequence with adenosine or ASP (preferably ATP), isolating a
 CC subpopulation by partitioning DNA molecules which specifically bind the
 CC adenosine or ASP, amplifying the subpopulation in vitro and repeating the
 CC process 4 times to obtain a single stranded DNA molecule capable of

CC binding adenosine or ASP, i.e. Systematic Evolution of Ligands by
 CC Exponential enrichment (SELEX). Catalytic DNA produced using the method
 CC can be used as in vitro or in vivo catalysts, or to detect the presence
 CC of the ligand. They may also be used in assays to detect molecules
 CC modified by the DNA, which are not themselves ligands, e.g. DNA
 CC phosphorylated by a polynucleotide kinase catalyst. The DNA molecule has
 CC significant advantages over ligand binding and catalytic RNA in terms of
 CC stability and synthesis cost
 XX

SQ Sequence 14 BP; 5 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 180 CTTCTCCGCTA 191
 Db 13 CTTCTCCGCTA 2

RESULT 94
 AAQ40305
 ID AAQ40305 standard; cDNA; 15 BP.
 AC AAQ40305;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-AUG-1993 (first entry)
 DE Sequence of PCR primer oligo lambda-F for amplification of a fragment of
 DE PTOM38 encoding glyceraldehyde-3-phosphate dehydrogenase (GPDH).
 XX
 KM Glyceraldehyde-3-phosphate dehydrogenase; inhibitor; antisense RNA;
 KM fruit; ripening; se.
 XX
 OS Synthetic.
 XX
 PN WO9307275-A1.
 XX
 PD 15-APR-1993.
 XX
 PF 01-OCT-1992; 92WO-GB001806.
 XX
 PR 03-OCT-1991; 91GB-00021074.
 XX
 PA (ICIL) IMPERIAL CHEM IND PLC.
 XX
 PI Bird CR, Grierson D, Ray JA, Schuch W;
 XX
 DR WPI; 1993-134464/16.
 XX
 PT DNA constructs for anti-sense inhibition of GPDH in plants - used to
 PT modify ripening characteristics of climacteric fruit via inhibition of
 PT respiration.
 XX
 PS Example; Fig 2; 22pp; English.

CC The cDNA sequence is a fragment of cDNA for tomato cytosolic GPDH used in
 CC a novel DNA construct under control of transcriptional initiation region
 CC operative in plants. The construct is used to produce plants in which
 CC GPDH expression is modified; in partic. the constructs produce antisense
 CC RNA to down regulate expression. The transcriptional initiation region is
 CC a constitutive promoter. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 246 CTCCTGGAGCCC 257
 Db 3 CTCCTGGAGCCC 14

RESULT 95
AAQ89599
ID AAQ89599 standard; DNA; 15 BP.
XX
AC AAQ89599;
XX
DT 06-NOV-1995 (first entry)
XX
DE Lambda-gt11 5' sequencing primer.
XX
KM Kappa-casein; milk protein; primer; polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN US5391497-A.
XX
PD 21-FEB-1995.
XX
PF 13-OCT-1992; 92US-00962569.
XX
PR 13-OCT-1992; 92US-00962569.
XX
PA (COLS) UNIV COLORADO FOUND INC.
XX
PI Ham RG, Jeffers KF, Menon RS, Chang Y;
XX
DR WPI; 1995-160470/21.
DR P-PADB; AAR72697.
XX
PT DNA encoding human kappa-casein - used for the prodn. of large amts. of
PT highly purified kappa-casein milk protein for infant use.
XX
PS Example B; Col 11; 14pp; English.
XX
CC A commercial cDNA library prepd. in lambda gt11 from mRNA obt'd. from
CC human breast tissue removed during the third trimester of pregnancy was
CC screened with rabbit anti-bovine kappa-casein cDNA. The cDNA insert of a
CC recombinant phage was amplified by PCR using the primer given in AAQ89599
CC (located 13-27 bp upstream of the EcoRI site of lambda gt11) and AAQ89600
CC (located 8-27 bp downstream of the EcoRI site)
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14
RESULT 96
AAT32436
ID AAT32436 standard; DNA; 15 BP.
XX
AC AAT32436;
XX
DT 30-SEP-1996 (first entry)
XX
DE PCR primer lambda gt11 forward.
XX
KM Wasp; venom; neurotoxin; insecticide; biological control agent;
KM Lepidoptera; insect; Bracon hebetor; polymerase chain reaction; PCR;
KM primer; ss.
XX
OS Synthetic.
XX
PN WO9616171-A1.
XX
PD 30-MAY-1996.

XX
PF 21-NOV-1995; 95WO-GB002720.
XX
PR 22-NOV-1994; 94GB-00023540.
PR 19-JAN-1995; 95GB-00001074.
PR 29-JUN-1995; 95GB-00013293.
XX
PA (ZENE) ZENECA LTD.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Windass JD, Duncan RE, Baule VJ, Christian PD;
XX
DR WPI; 1996-268607/27.
XX
PT Bracon hebetor toxins and DNA encoding them - useful in biological
PT control agents to combat insect pests.
XX
PS Example 4; Page 20; 83pp; English.
XX
CC The PCR primer pair lambda gt11 forward (AAT32436) and lambda gt11
CC reverse (AAT32437) were used to screen for the presence of a cDNA insert
CC in plaque-purified phage obt'd. from a Bracon hebetor wasp cDNA library.
CC The primers are specific for phage lambda gt11 and flank the EcoRI
CC cloning site. cDNA clone pBrtX-1(a)1.1 (AAT32438) was identified that
CC codes for the toxin (a) subunit (AAR99568) of the wasp neurotoxin BrtX-
CC 1. This can be utilised in breeding of biological control agents used to
CC combat insect pests
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14
RESULT 97
AA56935/C
ID AA56935 standard; DNA; 15 BP.
XX
AC AA56935;
XX
XX 16-OCT-2003 (revised)
DT 15-JUL-1999 (first entry)
XX
DE HIV-1 proviral DNA fragment 18.
XX
KM DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;
KM viral DNA-binding agent; solid support; primer; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9531434-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US006379.
XX
PR 13-MAY-1994; 94US-00242664.
XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (ZMBI-) ZW BIOMEDICAL RES AG.
XX
PI Watanabe KA, Ren W, Weil R;
XX
DR WPI; 1996-010846/01.
XX
PT Derivatised solid supports and reagents for oligo:nucleotide synthesis -
PT and new oligo:nucleotide phosphoramidate conjugates.

PS Disclosure; Page 46; 68bp; English.

XX This invention describes novel derivatised solid supports of formula S'-L

CC -2-CH₂CH₂-R, where: S' = a solid support; L = a bond or an (in)organic

CC linker; Z = SO₂ or S-S; R = OH, an H-phosphonate, alkaneophosphonate,

CC phosphorotriester, phosphate triester, phosphite diester, phosphotriate,

CC phosphorodithiophate, phosphoramidate or phosphoramidite group, OR1, SR1,

CC an optionally substituted or modified nucleotide (N'), or an

CC oligonucleotide of formula (N')GR₂; G = 1-200; R₁ = a protecting group;

CC R₂ = an H-phosphonate, alkaneophosphonate, phosphotriester, phosphite

CC triester, phosphate diester, phosphorothioate, phosphorodithiophate,

CC phosphoramidate or phosphoramidite group, OR1, SR1 or

CC OP(OCH₂CH₂CH₂CH₂CH₂CH₂OR1). Also mentioned are compounds of formula

CC R₃CH₂CH₂CH₂CH₂CH₂CH₂OR₄, where: R₃ = a protecting group; and R₄ = OH or an H-

CC phosphonate, alkaneophosphonate, phosphotriester, phosphite triester,

CC phosphite diester, phosphorothioate, phosphorodithiophate, phosphoramidate

CC or phosphoramidite group. Also claimed are new phosphoramidates, a

CC process for preparing an oligonucleotide 5'-phosphate, a process for

CC preparing a solid support useful for preparation of an oligonucleotide 3'

CC -phosphate, a process for preparing an oligonucleotide 3'-phosphate and a

CC process for preparing an oligonucleotide 3',5'-diphosphate. The

CC oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNA-

CC targeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNA-

CC cleaving or -binding agents. The process for preparing oligonucleotide

CC 3',5'-diphosphates is simple and suitable for use in automatic DNA

CC synthesis. This sequence represents a fragment of the HIV-1 provirus

CC genome, used to describe the method of the invention. (Updated on 16-OCT-

CC 2003 to standardise OS field)

CC XX

SQ Sequence 15 BP; 9 A; 1 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCTCCTC 186

DB 13 TTGCTCTTCTCCTC 2

RESULT 98

AA114822

ID AA114822 standard; DNA; 15 BP.

XX

XX AA114822;

AC

XX

DT 17-SEP-1996 (first entry)

XX

DE Lambda gtl1 flanking sequence 5' primer.

XX

KM Histocyte-secreted factor; HSF; cytokine; antitumour; tumour; therapy;

KM polymerase chain reaction; PCR; primer; ss.

OS Synthetic.

XX

PN MO9613586-A2.

XX

PD 09-MAY-1996.

XX

PF 26-OCT-1995; 95WO-0P002200.

XX

PR 26-OCT-1994; 94JP-00297780.

XX

PA (SATC/) SATOMI N.

XX

PI Satomi N;

XX

DR WPI; 1996-239499/24.

XX

PT DNA encoding histocyte-secreted factor and its variants - useful as an

PT anti-tumour agent and for studying tumour regression, having low

PT cytotoxicity compared to TNF.

XX

PS Example 6; Page 30; 52bp; English.

XX

CC Lambda gtl1 5' (AA114822) and 3' (AA114823) primers were used in a lambda

CC gtl1 cDNA insert screening kit to identify insert DNA in clones obtd. by

CC the PCR amplification of human histocytic lymphoma DNA from a lambda

CC gtl1 library. A genomic clone (AA114818) coding for human HSF (AAR96800),

CC a novel cytokine, was identified

XX

SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257

DB 3 CTCCTGAGGCC 14

RESULT 99

AA135227

ID AA135227 standard; DNA; 15 BP.

XX

AC AA135227;

XX

DT 05-DEC-1996 (first entry)

XX

DE Cytoplasmic antiprotease PCR primer ZC2683.

XX

KM Cytoplasmic antiprotease-2 protein; CAP-2; CAP-3; serpin;

KM serine protease inhibitor; antiinflammatory; apoptosis;

KM polymerase chain reaction; PCR; primer; ss.

XX

OS Synthetic.

XX

PN MO9624650-A2.

XX

PD 15-AUG-1996.

XX

PF 02-FEB-1996; 96WO-US001288.

XX

PR 08-FEB-1995; 95US-00385500.

XX

PA (ZYMO) ZYMOGENETICS INC.

XX

XX Sprecher CA;

DR WPI; 1996-393014/39.

XX

PT Human cytoplasmic antiprotease-2 (CAP-2) and CAP-3 - serine protease

PT inhibitors useful in the purification of proteins and in the treatment of

PT inflammatory diseases and apoptosis.

XX

PS Example 1; Page 43; 50bp; English.

XX

CC PCR primers ZC2682 (AA135226) and ZC2683 (AA135227) anneal 5' and 3' to

CC the EcoRI cloning site of lambda gtl1. They were utilised in the PCR

CC amplification of cDNA inserts in clones that had been obtd. from a human

CC placenta cDNA library in lambda gtl1 using a partial clone as probe (see

CC also AA135222-25). 2 different PCR products were generated (AA135220-21)

CC that respectively coded for cytoplasmic antiproteases 2 and 3 (AAR99253

CC -54)

XX

SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257

DB 3 CTCCTGAGGCC 14

```

RESULT 100
AAV17170
ID AAV17170 standard; DNA; 15 BP.
XX
AC AAV17170;
XX
DT 18-JUN-1998 (first entry)
XX
DE Insecticidal toxin subunit cDNA amplifying primer 1.
XX
KW Insecticidal toxin; Bracon hebetor; insect control; pathogen;
XX recombinant baculovirus; PCR primer; ss.
XX
OS Synthetic.
XX Bracon hebetor.
XX
PN MO9744355-A1.
XX
PD 27-NOV-1997.
XX
PF 01-MAY-1997; 97WO-GE001205.
XX
PR 22-MAY-1996; 96GB-00010687.
XX 22-MAY-1996; 96GB-00010695.
XX 22-MAY-1996; 96GB-00010697.
XX 22-MAY-1996; 96GB-00010738.
XX 22-MAY-1996; 96GB-00010739.
XX 22-MAY-1996; 96GB-00010748.
XX
PA (ZENE) ZENECA LTD.
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
PI Duncan RE, Sumner M, Daly A, Christian PD, Windass JD,
PI Claudianos A;
XX
DR WPI; 1998-018430/02.
XX
PT New nucleic acid encoding a combination of insecticidal subunit(s) of
PT wasp toxin - and related transformed cells; insect pathogens and
PT combinations of proteins; useful as insecticides.
XX
PS Disclosure; Page 61; 84pp; English.
XX
CC This primer is used for PCR amplification of an insecticidal toxin
CC subunit cDNA of the invention. The specification provides a 1811 base
CC pair spliced RNA (AAV17183) derived from a Bracon hebetor genomic clone
CC that encodes at least two of the insecticidal toxin subunits shown in
CC sequences AAM52124-W52128. The spliced RNA can hybridise with extension
CC products prepared from a 564 base pair (AAV17145) template with 6
CC specified primers. A nucleic acid encoding at least one of the specified
CC subunits can be modified so that mRNA instability motifs and/or
CC fortuitous splice sites are removed, or insect-pest preference codons are
CC used, so that expression of this nucleic acid in insect cells yields
CC practically the same protein as unmodified nucleic acid in its endogenous
CC organism. The nucleic acid encoding an insecticidal toxin subunit can be
CC complementary to a sequence that hybridises under specified conditions to
CC any of sequences shown in AAV17145 to AAV17149. Cells transformed with
CC these nucleic acids, organisms regenerated from these cells and pathogens
CC containing these nucleic acids and insecticidal compositions comprising a
CC combinations of the toxin subunits are all used for control of insects.
CC The nucleic acids are used to produce recombinant baculoviruses for
CC insect control
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 257
Db 3 CTCCTGAGGCC 14

```

```

RESULT 101
AAV15707
ID AAV15707 standard; DNA; 15 BP.
XX
AC AAV15707;
XX
DT 03-JUL-1998 (first entry)
XX
DE Primer for recombinant mosquito salivary allergen rnaed a 3 cDNA.
XX
KW Recombinant; mosquito; salivary allergen; rnaed a 3; determination;
XX bite sensitivity; epi-cutaneous test; skin test; intradermal test;
XX allergy diagnosis; immunotherapy; desensitisation; PCR primer; ss.
XX
OS Synthetic.
XX Aedes aegypti.
XX
PN MO9804274-A1.
XX
PD 05-FEB-1998.
XX
PF 31-JUL-1997; 97WO-US013573.
XX
PR 31-JUL-1996; 96US-0023118P.
XX
PA (UTMA-) UNIV MANITOBA.
XX (KOHN/) KOHN K I.
XX
PI Peng Z, Simons F;
XX
DR WPI; 1998-130418/12.
XX
PT Recombinant mosquito salivary allergens for use in skin tests for
PT sensitivity - also as substrate for assaying allergen-specific
PT immunoglobulin and for de-sensitisation immuno-therapy.
XX
PS Example 4; Page 43; 82pp; English.
XX
CC The present sequence is a primer for the cDNA encoding the recombinant
CC mosquito salivary allergen rnaed a 3. rnaed a 3 can be used to determine
CC sensitivity to mosquito bites by epi-cutaneous or intradermal testing, as
CC a substrate to which IgE/G bind (e.g. for mosquito allergy diagnosis) and
CC (based on the results of the skin tests) for immunotherapy
CC (desensitisation)
XX
SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGGCC 257
Db 3 CTCCTGAGGCC 14

```

OS Synthetic.
 OS Aedes aegypti.
 XX
 XX MO925826-A1.
 XX
 PD 27-MAY-1999.
 XX
 PF 13-NOV-1998; 98WO-IB001961.
 XX
 PR 13-NOV-1997; 97US-0065402P.
 XX
 PA (UTMA-) UNIV MANITOBA.
 XX
 PI Simons FER, Peng Z;
 XX
 DR WPI; 1999-347473/29.
 XX
 PT Mosquito extract consisting of antigens to allergens in mosquito saliva.
 XX
 PS Example 4; Page 41; 77pp; English.
 XX
 CC The present invention describes a mosquito extract consisting essentially
 CC of antigens related solely to allergens in mosquito saliva. The isolated
 CC and purified recombinant mosquito salivary antigens are for use in skin
 CC test, immunoassays and immunotherapy for allergic reactions to mosquito
 CC bites. The mosquito extract consists essentially of these antigens to
 CC allergens in mosquito saliva. The assays are applicable to patients
 CC presenting with rashes and other symptoms after mosquito bites,
 CC especially those with erythema, edema and induration, pain or itch at
 CC the site(s) of mosquito bite(s), with or without fever. These patients
 CC are at risk for severe localized inflammatory reactions and systemic
 CC reactions to mosquito bites. The present sequence represents a PCR primer
 CC for an Aed a 3 cDNA clone AA22, which was isolated from Aedes aegypti
 CC (mosquito) saliva in an example from the present invention for the
 CC isolation of a cDNA encoding a 30 kDa IGF-binding protein
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 246 CTCCTGGAGCCC 257
 DB 3 CTCCTGGAGCCC 14
 RESULT 103
 AA239756
 ID AA239756 standard; DNA; 15 BP.
 XX
 AC AA239756;
 XX
 DT 06-MAR-2000 (first entry)
 XX
 DE Human CAP DNA specific primer ZC2683.
 XX
 KW Caspase; serpin; inflammation; apoptosis; lung disease; human; CAP;
 KW neurodegenerative disease; heart; liver tissue; Alzheimer's disease;
 KW Parkinson's disease; amyotrophic lateral sclerosis; injury; trauma;
 KW hypoxia-ischaemia; cytoplasmic antiprotease protein; PCR primer;
 KW nociceptive; neuroprotective; vasotropic; tranquilizer; vulnery; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9957273-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 27-APR-1999; 99WO-US008949.
 XX
 PR 04-MAY-1998; 98US-00072275.

XX
 PA (ZYMO) ZYMOGENETICS.
 XX
 PI Sprecher CA, Foster DC, Jaepers SR;
 XX
 DR WPI; 2000-062146/05.
 XX
 PT Method for treating disease or symptoms of a disease mediated by a
 PT caspase.
 XX
 PS Example 1; Page 63; 65pp; English.
 XX
 CC The invention provides a method for treating a disease mediated by a
 CC caspase in an individual. The method comprises administering a
 CC composition comprising a gene coding for an intracellular mammalian
 CC serpin in an amount sufficient to inhibit activity of the caspase upon
 CC transient expression of the gene in a target tissue affected by the
 CC disease, where the disease or the symptoms are treated. The method can be
 CC used for decreasing inflammation, for modulating apoptosis, for treating
 CC a lung disease, and for treating a neurodegenerative disease. The
 CC inflammation and apoptosis that can be treated are particularly in heart
 CC or liver tissue. It can be used for treating Alzheimer's disease,
 CC Parkinson's disease, amyotrophic lateral sclerosis, and acute injury such
 CC as hypoxia-ischaemia or trauma. Sequences AA239755-56 represent PCR
 CC primers specific for the human cytoplasmic antiprotease protein (CAP)
 XX
 SQ Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 3; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 246 CTCCTGGAGCCC 257
 DB 3 CTCCTGGAGCCC 14
 RESULT 104
 AAH21253
 ID AAH21253 standard; DNA; 15 BP.
 XX
 AC AAH21253;
 XX
 DT 13-SEP-2001 (first entry)
 XX
 DE Human Kv4.1 screening amplicon SEQ ID 10.
 XX
 KW Human; Kv4.1; potassium channel protein; Kv4.2; autism; epilepsy;
 KW neurodegenerative disease; ischemia; stroke; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; cardiac arrhythmia; memory;
 KW learning capacity; protein kinase activator; anti-arrhythmic; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19963612-A1.
 XX
 PD 12-JUL-2001.
 XX
 PF 29-DEC-1999; 99DE-01063612.
 XX
 PR 29-DEC-1999; 99DE-01063612.
 XX
 PA (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
 XX
 DR WPI; 2001-426637/46.
 XX
 PT New potassium channel subunit proteins, useful for identifying and
 PT testing potential pharmaceuticals, e.g. anti-arrhythmic or neurological
 PT agents.
 XX
 PS Example 2; Page 26; 50pp; German.
 XX
 CC This invention describes a novel potassium channel protein (1) that is

CC either human Kv4.1 or Kv4.2. Eukaryotic cells that express potassium
CC channels containing (I) are used to identify and test: (i) compounds for
CC treatment of neurodegenerative diseases (autism, epilepsy, ischemia,
CC stroke; Alzheimer's, Parkinson's and Huntington's diseases) or cardiac
CC arrhythmia, or those that improve learning capacity and memory; and (ii)
CC activators of protein kinases. Host cells that express (i) can identify
CC agents that do not interact significantly with channels and control I_{to}
CC (a quickly activated transient current), so lack the side effects of
CC known anti-arrhythmic agents. They also eliminate, or reduce, the need
CC for testing on organ cultures

SO Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGGCC 257
DB 3 CTCCTGAGGCC 14

RESULT 105
AAFS0004/c
ID AAF50004 standard; DNA; 15 BP.

AC AAF50004;
DT 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #964.

DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR.

XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,

CC ichthyosis, pteryiasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia

SO Sequence 15 BP; 0 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376
DB 13 AGCCCGAGGGGC 2

RESULT 106
AAFS0002/c
ID AAF50002 standard; DNA; 15 BP.

AC AAF50002;
DT 30-MAR-2001 (first entry)
XX
XX IGF-I oligonucleotide #962.

DE Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pteryiasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.

OS Homo sapiens.

XX WO200078341-A1.

XX 28-DEC-2000.

XX 21-JUN-2000; 2000WO-AU000693.

XX 21-JUN-1999; 99US-0140345P.

XX (MURD-) MURDOCH CHILDRENS RES INST.

XX Wraight CJ, Werther GA, Edmondson SR.

XX WPI; 2001-041421/05.

PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.

XX Example 8; Page 67; 201pp; English.

CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pteryiasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic

CC	disease kidney disease, hyperproliferation of the inside of blood
CC	vessels or any other hyperplasia
XX	
XX	Sequence 15 BP; 1 A; 6 C; 5 G; 3 T; 0 U; 0 Other;
QY	
	365 AGCCCCGAGGGC 376
	15 AGCCCGAGGGC 4
Db	
	Query Match 2.0%; Score 12; DB 4; Length 15;
	Best Local Similarity 100.0%; Pred. No. 1.2e+05;
	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
RESULT 107	
AAF5003/c	
ID	AAF50003 standard; DNA; 15 BP.
AC	AAF50003;
DT	30-MAR-2001 (first entry)
XX	
DE	IGF-1 oligonucleotide #963.
XX	
KM	Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KM	cytostatic; dermatological; cardiac; virucide; ophthalmological; keloid;
KM	skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KM	IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM	growth factor mediated cell proliferation; ichthyosis; seborrhoea; ruba;
KM	keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM	hyperneovascular condition; hyperplasia; kidney disease;
KM	neovascular condition of the retina; ss.
OS	Homo sapiens.
PN	WO200078341-A1.
XX	
FD	28-DEC-2000.
XX	
PF	21-JUN-2000; 2000WC-AU000693.
XX	
PR	21-JUN-1999; 99US-0140345P.
XX	
PA	(MURDOCH CHILDRENS RES INST.
XX	
P1	Wraight CJ, Werther GA, Edmondson SR;
XX	
XX	WPI; 2001-041421/05.
DR	
XX	
PT	Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT	UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT	inhibits or reduces growth factor mediated cell proliferation and/or
PT	inflammation.
XX	
XX	Example 8; Page 67; 201pp; English.
CC	
CC	The present invention relates to a method for ameliorating the effects of
CC	skin disorders. The method comprises contacting the skin with an
CC	antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC	receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC	inhibiting or reducing growth factor mediated cell proliferation,
CC	inflammation and/or other disorders. The present sequence is an
CC	oligonucleotide which can be used to design the antisense
CC	oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC	P45161). The method is useful for ameliorating the effects of psoriasis,
CC	ichthyosis, pityriasis, ruba, pilaris, seborrhoea, keloids, keratosis,
CC	hyperplasia, scleroderma, warts, benign growths, cancers of the skin, a
CC	hyperneovascular condition such as a neovascular condition of the retina,
CC	brain or skin, growth factor-mediated malignancies, other sclerotic
CC	disease, kidney disease, hyperproliferation of the inside of blood
CC	vessels or any other hyperplasia
XX	
XX	
Sequence 15 BP; 0 A; 6 C; 5 G; 4 T; 0 U; 0 Other;	

Query Match Similarity 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 AGCCCGAGGGGC 376
|||
DB 14 AGCCCGAGGGGC 3

RESULT 108
ID AAF50005/c
AAF50005 standard; DNA; 15 BP.
AC AAF50005;
AT 30-MAR-2001 (first entry)
CT IGF-I oligonucleotide #965.
DE
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytoskeletal; dermatological; cardiac; vitruclide; ophthalmological; keloid;
KM skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KM growth factor mediated cell proliferation; ichthyosis; seborrhoea; rubra;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KM hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.

OS Homo sapiens.
XX
XX MO200078341-A1.
PN
XX 28-DEC-2000.
PD
XX 21-JUN-2000; 2000MO-AU000693.
PF
XX 21-JUN-1999; 99US-014034SP.
PR
XX (MURD-) MURDOCH CHILDRENS RES INST.
PA
XX Wraight CJ, Werther GA, Edmondson SR;
PI WPI; 2001-041421/05.
DR
XX

Ameliorating the effects of a disorder, e.g. psoriasis, by administering UV (ultra-violet) treatment (optional) and an antisense nucleic acid that inhibits or reduces growth factor mediated cell proliferation and/or inflammation.

Example 8; Page 67; 201pp; English.

The present invention relates to a method for ameliorating the effects of skin disorders. The method comprises contacting the skin with an antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1 receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of inhibiting or reducing growth factor mediated cell proliferation, inflammation and/or other disorders. The present sequence is an oligonucleotide which can be used to design the antisense oligonucleotides of the present invention (see AAF45151 and AAF45153-P45161). The method is useful for ameliorating the effects of psoriasis, ichthyosis, pityriasis, rubra, pilaris, seborrhoea, keloids, keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the skin, a hyperneovascular condition such as a neovascular condition of the retina, brain or skin, growth factor-mediated malignancies, other sclerotic disease, kidney disease, hyperproliferation of the inside of blood vessels or any other hyperplasia

Sequence 15 BP; 1 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match Similarity 2.0%; Score 12; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376
 |||||
 DB 12 AGCCCGAGGGGC 1

RESULT 109

ACD26289
 ID ACD26289 standard; DNA; 15 BP.

AC ACD26289;
 XX

DT 03-SEP-2003 (first entry)

DE Gene chip associated oligonucleotide #1.

XX Gene chip; ss; hairpin; full match; single-point mismatch.

OS Unidentified.

XX CN1373228-A.
 XX

PD 09-OCT-2002.
 XX

PF 22-MAR-2002; 2002CN-00116302.

XX 22-MAR-2002; 2002CN-00116302.

XX (UYBE-) UNIV BEIJING.

PI Zhao X, Wei F, Sun B;
 XX

DR WPI; 2003-141480/14.
 XX

PT Gene chip for recognizing full match and single-point mismatch, comprises
 PT hairpin-shaped probes having a detecting region and a stem region.

XX Disclosure; Page 6 (Disclosure); 11pp; Chinese.

XX The invention relates to a gene chip which is composed of a chip
 CC substrate and oligomeric nucleic acid probes fixed on the substrate. The
 CC probe is composed of a detecting region and a stem region, where a
 CC hairpin-shaped dual-chain structure is formed by the oligomeric nucleic
 CC acid sequence and the one matched with it. Controlling the electric
 CC potential of the gene chip can further optimize hybridisation conditions.
 CC Its advantages are repeated application, low cost and the power for
 CC recognizing full match and single-point mismatch. The present sequence
 CC represents the gene chip associated oligonucleotide #1

XX Sequence 15 BP; 4 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
 |||||

DB 4 ATGACCGGAGG 15

RESULT 110

AAQ6708/c
 ID AAQ6708 standard; DNA; 16 BP.

XX AAQ6708;
 AC

DT 22-DEC-1994 (first entry)

XX Primer to amplify HHV6 derived sequences.

DE HHV6; Human Herpes Virus 6; Primers; Probes; PCR; amplify;
 XX polymerase chain reaction; ss.

XX

OS Synthetic.

XX JP06133799-A.
 XX

PD 17-MAY-1994.
 XX

PF 27-OCT-1992; 92JP-00311416.

XX 27-OCT-1992; 92JP-00311416.

XX (KOKU-) KOKUSAI SHIYAKU KK.
 XX

DR WPI; 1994-196175/24.
 XX

XX HHV-6 derived nucleotide(s) - useful for identification of HHV-6 DNA.

XX Claim 4; Page 2; 13pp; Japanese.

CC The inventors provide human Herpes virus 6 derived nucleotide sequences
 CC useful for identification of HHV-6 DNA. AAQ6705-12 are primer set 1 (1),
 CC are used in the invention

XX Sequence 16 BP; 5 A; 2 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 CATGAATAATCA 507
 |||||

DB 12 CATGAATAATCA 1

RESULT 111

ACA58181/c
 ID ACA58181 standard; DNA; 16 BP.

XX ACA58181;
 AC

DT 09-JUN-2003 (first entry)

XX Human familial bipolar affective disorder chromosome marker #129.

XX Human; genotype determination; familial bipolar affective disorder;
 XX chromosomal region linked; locus associated with resistance; D4S402;
 XX D4S42; D4S431; D4S404; D1S394; D1S29; chromosome marker; primer; ss.

XX Homo sapiens.

OS

XX US2002192655-A1.
 XX

PD 19-DEC-2002.
 XX

PF 13-JUN-2001; 2001US-00881012.

XX 29-MAR-1996; 96US-0014334P.
 XX 20-OCT-1997; 97US-0062924P.
 XX 19-OCT-1998; 98US-00175158.

XX (GINN/) GINN S I.
 XX (EGEL/) EGELAND J A.
 XX (PAUL/) PAUL S M.

XX Ginn S I, Egeland J A, Paul S M;
 PI

XX WPI; 2003-352708/33.

XX Determining a genotype associated with increased or decreased resistance
 PT to familial bipolar affective disorder in a family comprises determining
 PT the genotype of e.g., chromosomal regions D4S402 and D4S424.

XX Disclosure; Page 11; 79pp; English.

XX

XX

XX

XX

CC The present invention relates to a method of determining a genotype
 CC associated with increased or decreased resistance to familial bipolar
 CC affective disorder. The method comprises determining the genotype with at
 CC least one marker of at least one chromosomal region linked to a locus
 CC associated with resistance to bipolar affective disorder, where the
 CC chromosomal regions are included of and localised between D4S402 and
 CC D4S424, D4S431 and D4S404, or D11S394 and D11S29. The invention also
 CC discloses a kit for determining a genotype associated with increased or
 CC decreased resistance to familial bipolar affective disorder, where the
 CC kit comprises markers for two or more of the chromosomal regions cited.
 CC The method and kit are useful for determining a genotype associated with
 CC increased or decreased resistance to familial bipolar affective disorder
 CC in a family affected by bipolar affective disorder, for determining the
 CC contribution of these chromosomal regions to bipolar affective disorder
 CC in an affective family member, and for assessing an increased or
 CC decreased risk of developing bipolar illness for a tested individual from
 CC an affected family. AC458053-AC458292 represent primers used in the
 CC present invention
 CC
 XX
 SQ Sequence 16 BP; 5 A; 3 C; 7 G; 1 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 241 TTCACTCTCTGG 252
 Db 15 TTCACTCTCTGG 4
 XX
 RESULT 112
 AAQ26187
 ID AAQ26187 standard; DNA; 17 BP.
 AC AAQ26187;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-JAN-1993 (first entry)
 XX
 DE HLA-DR beta sub-type tailed probe DRB3 hybridising region.
 XX
 KM Tissue typing; identity determination; disease susceptible; ss.
 XX
 OS Synthetic.
 XX
 PN WO9210589-A1.
 XX
 PD 25-JUN-1992.
 XX
 PF 06-DEC-1991; 91WO-US009294.
 XX
 PR 06-DEC-1990; 90US-00623098.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;
 PI Apple RJ;
 XX
 DR WPI; 1992-234644/28.
 XX
 PT Method for determining HLA-DR beta sub-type in DNA sample - comprises
 PT amplification and hybridisation with probes and primers, useful in tissue
 PT typing.
 XX
 PS Example; Page 39; 90pp; English.
 XX
 CC The sequence is that of the hybridising region of tailed probe DRB3 for
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
 CC sample. The method allows specific nucleic acid sequences of the second
 CC exon of HLA-DR beta genes to be amplified then probed for identification
 CC of polymorphic sequences. The amplified DNA is useful for typing
 CC homozygous or heterozygous samples from a variety of sources and for
 CC detecting allelic variants not distinguishable by serological methods.

CC The typing system can be used in a reverse dot blot format which is
 CC simple and rapid to perform, produces detectable signals in minutes and
 CC can be utilised in tissue typing, determination of individual identity
 CC and identifying disease susceptible individuals. See also AAQ26092-
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 244 ACCTCTGGAGC 255
 Db 1 ACCTCTGGAGC 12
 XX
 RESULT 113
 AAQ26166
 ID AAQ26166 standard; DNA; 17 BP.
 AC AAQ26166;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-JAN-1993 (first entry)
 XX
 DE HLA-DR beta sub-type tailed probe DRB1 hybridising region.
 XX
 KM Tissue typing; identity determination; disease susceptible; ss.
 XX
 OS Synthetic.
 XX
 PN WO9210589-A1.
 XX
 PD 25-JUN-1992.
 XX
 PF 06-DEC-1991; 91WO-US009294.
 XX
 PR 06-DEC-1990; 90US-00623098.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;
 PI Apple RJ;
 XX
 DR WPI; 1992-234644/28.
 XX
 PT Method for determining HLA-DR beta sub-type in DNA sample - comprises
 PT amplification and hybridisation with probes and primers, useful in tissue
 PT typing.
 XX
 PS Example; Page 38; 90pp; English.
 XX
 CC The sequence is that of the hybridising region of tailed probe DRB1 for
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
 CC sample. The method allows specific nucleic acid sequences of the second
 CC exon of HLA-DR beta genes to be amplified then probed for identification
 CC of polymorphic sequences. The amplified DNA is useful for typing
 CC homozygous or heterozygous samples from a variety of sources and for
 CC detecting allelic variants not distinguishable by serological methods.
 CC The typing system can be used in a reverse dot blot format which is
 CC simple and rapid to perform, produces detectable signals in minutes and
 CC can be utilised in tissue typing, determination of individual identity
 CC and identifying disease susceptible individuals. See also AAQ26092-
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 17 BP; 3 A; 5 C; 7 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 244 ACCTCTGGAGC 255

Db 1 ACCTCTGTGAGC 12

RESULT 114

ID AAO92156 standard; DNA; 17 BP.

XX AAO92156;

DT 11-JUN-1996 (first entry)

XX p53 detection probe, (codon 245 GGC to TGC).

XX Primer; polymerase chain reaction; amplify; mutant; K-ras; PCR;

XX flanking region; amplification; probe; detection; sputum; diagnosis;

XX benign; malignant; neoplasm; lung; lung cancer; head; neck; ss.

XX Synthetic.

XX WO9513397-A1.

XX 18-MAY-1995.

XX 10-NOV-1994; 94WO-US012947.

XX 12-NOV-1993; 93US-00152313.

XX (UYUO) UNIV JOHNS HOPKINS SCHOOL MED.

XX Sidransky D;

XX WPI; 1995-194114/25.

XX Detecting target nucleic acid in mammalian sputum - particularly for

XX diagnosis of lung neoplasia involving mutation(s) in the K-ras oncogene

XX or p53 tumour suppressor.

XX Example 1; Page 32; 122pp; English.

XX The sequences given in AAO92112-211 are probes which were used in the

XX detection of a mutant p53 gene sequence. The DNA to be detected is

XX amplified using PCR and then these probes which are pref. labeled using

XX 32-P gamma-ATP are used to detect the mutant sequences. The primers and

XX probes given in AAO92098-219 are used in the method of the invention for

XX detecting mammalian target DNA in sputum samples. Analysis of the target

XX DNA is used to diagnose benign or malignant neoplasms of the lung. It is

XX also useful for screening people at high risk or for monitoring progress

XX of treatment for lung neoplasms. The method is based on the discovery that

XX mutant target DNA associated with lung cancer is present at detectable

XX levels in sputum. Cells shed into sputum from head and neck cancers may

XX also be detected

XX Sequence 17 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 2; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Human; IL-2 receptor g-chain; interleukin 2 receptor gamma chain;

XX hammerhead ribozyme; hairpin ribozyme; substrate; expression; cancer;

XX autoimmune disease; psoriasis; allergy; inflammatory disease;

XX graft rejection; ss.

XX Synthetic.

XX Canis sp.

XX WO9824913-A2.

XX 11-JUN-1998.

XX 02-DEC-1997; 97WO-US021748.

XX 03-DEC-1996; 96US-00758306.

XX (RIBO-) RIBOZYME PHARM INC.

XX Stinchcomb DT, Mcswiggen JA;

XX WPI; 1998-333332/23.

XX Ribozymes targeted to interleukin 2 - useful for treating e.g. cancer,

XX autoimmune disease and allergies.

XX Claim 4; Page 47; 61pp; English.

XX The present sequence invention describes ribozymes targeted to modulate

XX the synthesis and/or expression of interleukin (IL)-2R gamma encoded RNA.

XX AAV93889 to AAV94574 represent specifically claimed ribozymes, and

XX AAV94575 to AAV95260 represent specifically claimed substrate sequences

XX from the present invention. The ribozymes can be used for the treatment

XX of, e.g. graft rejection, autoimmune disease, cancer, psoriasis, allergy

XX and other inflammatory conditions. The ribozymes are also used to induce

XX tolerance in a recipient to alloantigen from a donor

XX Sequence 17 BP; 3 A; 3 C; 10 G; 0 T; 1 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 2; Length 17;

XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 248 CCTGAGCCCT 259

XX 13 CCTGAGCCCT 2

XX RESULT 116

XX AAA18564/c

XX ID AAA18564 standard; RNA; 17 BP.

XX AAA18564;

XX 19-JUN-2000 (first entry)

XX Human TIR-2 substrate sequence SEQ ID NO:1790.

XX Human; aryl hydrocarbon nuclear transport; ANRT; TIR-2; angiogenesis;

XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;

XX hammerhead ribozyme; angiogenic factor; cytoabatic; antidiabetic;

XX ophthalmologic; antiinflammatory; antiaesthetic; antiporiatic; ARMD;

XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;

XX age related macular degeneration; inflammation; neovascular glaucoma;

XX myopic degeneration; psoriasis; verruca vulgaris; angiodioma;

XX tuberculous scleriosis; pot-wine stain; Sturge Weber syndrome;

XX Kippel-Trennauy-Weber syndrome; Osler-Weber-Rendu syndrome; ss.

XX Homo sapiens.

XX WO9950403-A2.

XX 07-OCT-1999.

XX Canine IL-2 receptor g-chain substrate position 1021.

```

XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA,
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 56; Page 103; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 3 A; 4 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 249 CTGAGCCCTG 260
XX |||||
XX 12 CTGAGCCCTG 1
XX
XX RESULT 117
XX ID AAA20707
XX AAA20707 standard; RNA; 17 BP.
XX
XX AAA20707;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:3933.
XX
XX Human; aryl hydrocarbon nuclear transporter; ARNT, Tie-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;
XX Kippel-Trenunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX

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OS Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswigen JA,
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX
XX Claim 55; Page 162; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT,
XX integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 5 A; 4 C; 0 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 58.3%; Pred. No. 1.2e+05;
XX Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX 35 TTTCACATTC 46
XX ::|||::|
XX 6 UUAACCAUUC 17
XX
XX RESULT 118
XX ID AAV91124/c
XX AAV91124 standard; RNA; 17 BP.
XX
XX AAV91124;
XX
XX 18-FEB-1999 (first entry)
XX
XX Human C-raf target site nucleotide position 1289.
XX
XX Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
XX target; substrate; catalyst; modulation; expression; Raf gene; delivery;
XX screening; identification; synthesis; deprotection; purification; cancer;
XX inflammation; psoriasis; non-hepatic ascites; infection; genetic drift;
XX restenosis; rheumatoid arthritis; ss.
XX

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XX OS Homo sapiens.
XX PN MO9850530-A2.
XX PD 12-NOV-1998.
XX PF 05-MAY-1998; 98WO-US009249.
XX PR 09-MAY-1997; 97US-0046059P.
XX PR 09-JUN-1997; 97US-0049002P.
XX PR 03-JUL-1997; 97US-0051718P.
XX PR 22-AUG-1997; 97US-0056808P.
XX PR 02-OCT-1997; 97US-0061321P.
XX PR 02-OCT-1997; 97US-0061324P.
XX PR 05-NOV-1997; 97US-0064866P.
XX PR 19-DEC-1997; 97US-0068212P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Jarvis T, Matulic-Adamic J, Reynolds M, Kistich K, Bellon L;
PI Parry T, Belgelman L, Mcswigen JA, Karpetsky A, Burgin A;
PI Thompson J, Workman CT, Beaudry A, Sweedler D;
DR WPI; 1999-009494/01.
XX PT Identifying new catalytic nucleic acid that modulates selected processes
XX PT - especially ribozymes that cleave Raf RNA for treating cancer,
XX PT restenosis, and also new ribozymes and modified nucleoside triphosphates
XX PT used as antiviral agents and synthons.
XX PS Claim 177; Page 149; 259pp; English.
XX CC A method has been developed for the identification of a nucleic acid
XX CC capable of modulating a process in a biological system. The method
XX CC comprises: (a) introducing into the system a random library of nucleic
XX CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
XX CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
XX CC in systems where modulation has occurred and/or determining the sequence
XX CC of at least part of the SBDs in such systems. Nucleic acid molecules with
XX CC endonuclease activity and catalytic activity, from the present invention,
XX CC are used to modulate gene expression in plant and mammalian cells and to
XX CC cleave target nucleic acid, particularly for treating systemic diseases
XX CC caused by specific RNA, e.g. cancer, inflammation, psoriasis, non-hepatic
XX CC acetosis and infection. They may also be used to detect genetic drift and
XX CC mutations in diseased cells and to determine c-raf RNA. Specifically NACs
XX CC with RNA-cleaving activity that modulate expression of the Raf gene, are
XX CC used to treat cancer, restenosis, psoriasis or rheumatoid arthritis, or
XX CC generally any condition associated with the level of c-raf. Introduction
XX CC of sugar/phosphate modifications increases stability against nuclease and
XX CC activity. AAV90922 to AAV93877 represent NACs that can be used in the
XX CC method, specifically for modulating the expression of a Raf gene
XX SO Sequence 17 BP; 5 A; 5 C; 4 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 170 TGGATTGCTCT 181
XX DB 12 TGGATTGCTCT 1
XX
XX RESULT 119
XX ID AAA36309 standard; DNA; 17 BP.
XX AC AAA36309;
XX XX
XX DT 26-JUL-2000 (first entry)
XX XX
XX DE Human genomic SNP allele specific oligonucleotide SEQ ID NO:375.
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XX OS Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
XX KM allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
XX KM genomic classification; identification; DNA fingerprinting;
XX KM tumour characterisation; hybridisation; ss.
XX OS Homo sapiens.
XX PN WO200018960-A2.
XX PD 06-APR-2000.
XX PF 24-SEP-1999; 99WO-US022283.
XX PR 25-SEP-1998; 98US-0101757P.
XX PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
XX PI Landers JE, Jordan B, Housman DE, Charest A;
XX DR WPI; 2000-293181/25.
XX PT Detection of single nucleotide polymorphisms in genomes by preparation
XX PT and analysis of reduced complexity genomes, useful for genotyping,
XX PT fingerprinting and determining allele frequency of SNPs.
XX PS Disclosure; Page 64; 11pp; English.
XX CC A method has been developed for detecting the presence or absence of a
XX CC single nucleotide polymorphism (SNP) allele in a genomic sample. The
XX CC method comprises preparing a reduced complexity genome (RCG) from the
XX CC genomic sample and analysing the RCG for the presence or absence of a SNP
XX CC allele. The method can be used to characterise a tumour, to generate a
XX CC genomic pattern for an individual genome or to generate a genomic
XX CC classification code for a genome. The method can be used to assess
XX CC whether a subject is at risk for developing a disease or to identify a
XX CC set of SNP alleles associated with a disease. The method can also be used
XX CC to perform linkage analysis. AAA5944 to AAA5947 represent sequences
XX CC used in the exemplification of the present invention. AAA5948 to
XX CC AAA5632 represent nucleotide sequences containing SNPs
XX SO Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 409 GCCATCATGACC 420
XX DB 5 GCCATCATGACC 16
XX
XX RESULT 120
XX ID AA288059 standard; DNA; 17 BP.
XX AC AA288059;
XX XX
XX DT 06-AUG-2003 (revised)
XX DT 20-APR-2000 (first entry)
XX DE Lentiviral proviral long terminal repeat DNA PCR primer #1.
XX KM Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX KM gene expression; PCR primer; ss.
XX OS Retroviridae.
XX PN WO200000600-A2.
XX XX
XX DT 06-JAN-2000.
XX PD
XX PF 26-MAY-1999; 99WO-US011516.
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XX 26-MAY-1998; 98US-0086635P.
XX (CHAN/) CHANG L.
XX Chang L;
XX WPI; 2000-137067/12.
XX
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example; Page 132; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
XX lentivirus that differs from the reference lentivirus at least in that:
XX (a) its major splice donor site is either deleted or is sufficiently
XX different from the reference lentivirus so that it is not a potential
XX site for homologous recombination; and (b) it lacks a functional major
XX packaging signal so that the introduced vector causes the host cell to
XX produce packaging vector particles comprising functional Gag and Pol
XX proteins. The vectors are useful for transforming (eukaryotic) cells to
XX express specific genes at high levels, e.g. for gene therapy. The
XX improved vectors are safer, yet permit increased efficiency of packaging
XX the recombinant viral genome and increased long-term gene expression.
XX These properties are required for gene therapy as a means of treating
XX infections and non-infectious diseases. Unlike other retroviruses, the
XX lentiviruses are able to infect non-dividing cells. The present sequence
XX represents a lentiviral proviral long terminal repeat DNA PCR primer
XX which is used in the exemplification of the present invention. (Updated
XX on 06-AUG-2003 to correct OS field.)
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 246 CTCTGTGAGCCC 257
XX |||||
XX 5 CTCTGTGAGCCC 16
XX
XX Db
XX
XX RESULT 121
XX ID AA288115 standard; DNA; 17 BP.
XX
XX AC AA288115;
XX
XX DT 20-APR-2000 (first entry)
XX
XX DE Hirt DNA PCR primer #1.
XX
XX KM Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX gene expression; PCR primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO200000600-A2.
XX
XX PD 06-JAN-2000.
XX
XX PF 26-MAY-1999; 99WO-US011516.
XX
XX PR 26-MAY-1998; 98US-0086635P.
XX
XX PA (CHAN/) CHANG L.
XX
XX PI Chang L;
XX
XX WPI; 2000-137067/12.
XX
```

```
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example 200; Page 213; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
XX lentivirus that differs from the reference lentivirus at least in that:
XX (a) its major splice donor site is either deleted or is sufficiently
XX different from the reference lentivirus so that it is not a potential
XX site for homologous recombination; and (b) it lacks a functional major
XX packaging signal so that the introduced vector causes the host cell to
XX produce packaging vector particles comprising functional Gag and Pol
XX proteins. The vectors are useful for transforming (eukaryotic) cells to
XX express specific genes at high levels, e.g. for gene therapy. The
XX improved vectors are safer, yet permit increased efficiency of packaging
XX the recombinant viral genome and increased long-term gene expression.
XX These properties are required for gene therapy as a means of treating
XX infections and non-infectious diseases. Unlike other retroviruses, the
XX lentiviruses are able to infect non-dividing cells. The present sequence
XX represents an oligonucleotide which is used in the exemplification of the
XX present invention
XX
XX Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX QY 246 CTCTGTGAGCCC 257
XX |||||
XX 5 CTCTGTGAGCCC 16
XX
XX Db
XX
XX RESULT 122
XX ID AA288064 standard; DNA; 17 BP.
XX
XX AC AA288064;
XX
XX DT 20-APR-2000 (first entry)
XX
XX DE MLV proviral long terminal repeat DNA PCR primer #2.
XX
XX KM Lentiviral vector; packaging; gag; pol; gene therapy; infection;
XX gene expression; PCR primer; ss.
XX
XX OS Murine leukemia virus.
XX
XX PN WO200000600-A2.
XX
XX PD 06-JAN-2000.
XX
XX PF 26-MAY-1999; 99WO-US011516.
XX
XX PR 26-MAY-1998; 98US-0086635P.
XX
XX PA (CHAN/) CHANG L.
XX
XX PI Chang L;
XX
XX WPI; 2000-137067/12.
XX
XX New packaging vector comprising a nucleotide sequence encoding Gag and
XX Pol proteins of a reference lentivirus useful for the delivery of non-
XX lentiviral genes to target cells.
XX
XX Example; Page 132; 311pp; English.
XX
XX The present invention describes a packaging vector (PV) comprising a
XX nucleotide sequence encoding Gag and Pol proteins of a reference
```

CC lentivirus that differs from the reference lentivirus at least in that:
 CC (a) its major splice donor site is either deleted or is sufficiently
 CC different from the reference lentivirus so that it is not a potential
 CC site for homologous recombination; and (b) it lacks a functional major
 CC packaging signal so that the introduced vector causes the host cell to
 CC produce packaging vector particles comprising functional gag and pol
 CC proteins. The vectors are useful for transforming (eukaryotic) cells to
 CC express specific genes at high levels, e.g. for gene therapy. The
 CC improved vectors are safer, yet permit increased efficiency of packaging
 CC the recombinant viral genome and increased long-term gene expression.
 CC These properties are required for gene therapy as a means of treating
 CC infectious and non-infectious diseases. Unlike other retroviruses, the
 CC lentiviruses are able to infect non-dividing cells. The present sequence
 CC represents an MLV proviral long terminal repeat DNA PCR primer which is
 CC used in the exemplification of the present invention

SQ Sequence 17 BP; 3 A; 7 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1,2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTGAGCC 257
 Db 5 CTCCTGAGCC 16

RESULT 123
 ABR02421/c
 ID ABR02421 standard; RNA; 17 BP.
 AC ABR02421;
 DT 12-MAR-2002 (first entry)
 XX Human NOGO Amberyze #93.
 DE Human NOGO Amberyze #93.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KM DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX MO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 XX 28-FEB-2000; 2000US-018516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX Blatt L, Mcswiggen J, Chowrira BM,
 XX WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX Claim 88; Page 132; 200P; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NCH motif) or
 CC an amberyze (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, mantle-cell
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an amberyze molecule of the invention

SQ Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1,2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCGAGG 373
 Db 15 CTGAGCCGAGG 4

RESULT 124
 ABR00051/c
 ID ABR00051 standard; RNA; 17 BP.
 AC ABR00051;
 DT 12-MAR-2002 (first entry)
 XX Human NOGO Hammerhead Ribozyme #51.
 XX
 XX Human NOGO Hammerhead Ribozyme #51.
 XX
 XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KM DNazyme; inozyme; G-cleaver; amberyze; zinzyme; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Homo sapiens.

OS Synthetic.
 XX
 PN MO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001MO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 66; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a hammerhead ribozyme of the invention
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 7 G; 0 T; 3 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 362 CTGAGCCGAGG 373
 DB 17 CTGAGCCGAGG 6

ID ABK00947 standard; RNA; 17 BP.
 XX
 AC ABK00947;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Inozyme #217.
 XX
 KW Human; ss; antisense therapy; cyostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNzyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN MO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001MO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 81; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more

CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an inozyme of the invention

XX Sequence 17 BP; 2 A; 5 C; 6 G; 0 T; 4 U; 0 Other;

Qy Query Match 2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 362 CTGAGCCCGAGG 373
12 CTGAGCCCGAGG 1

RESULT 126
ABK02420/c
ID ABK02420 standard; RNA; 17 BP.
XX
AC ABK02420;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Amberzyme #92.
XX
XX Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KM DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001MO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX
XX 28-FEB-2000; 2000US-0185516P.
XX
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX (BLAT) BLATT L.
XX
XX (MCSW/) MCSWIGGEN J.
XX
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM,
XX
XX WPI, 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 88; Page 132; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates

CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention

XX Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;

Qy Query Match 2.0%; Score 12; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 362 CTGAGCCCGAGG 373
16 CTGAGCCCGAGG 5

RESULT 127
ABK01846/c
ID ABK01846 standard; RNA; 17 BP.
XX
XX AC ABK01846;
XX
XX 12-MAR-2002 (first entry)
XX
XX DT Human NOGO Zinczyme #168.
XX
XX DE Human
XX
XX Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;
KM cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KM DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KM inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
OS Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001MO-US004273.
XX
XX

XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLAT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOM/) CHOMRIRA B M.
 PI Blatt L, Mcswiggen J, Chowrira BW,
 DR WPI; 2001-607195/69.
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 98; 200pp; English.
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zynzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapeutics. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOCO. The treatment may further comprise the use of one or more
 CC therapeutics. In particular, the NOCO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob,
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOCO expression. The present
 CC sequence is a zynzyme molecule of the invention
 XX
 SO Sequence 17 BP; 1 A; 6 C; 6 G; 0 T; 4 U; 0 Other;
 Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 CTGAGCCCGAGG 373
 DB 14 CTGAGCCCGAGG 3

RESULT 128
 ID ABA77345 standard; DNA; 17 BP.
 XX ABA77345;
 AC ABA77345;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE p53 mutation correcting oligonucleotide SEQ ID NO: 191.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thromboside;
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytosolic; antisticking; antineutrophilic; haemostatic;
 KW antileptemic; ss.
 XX
 XX Homo sapiens.
 OS
 XX MO200173002-A2.
 PN
 XX 04-OCT-2001.
 PD
 XX 27-MAR-2001; 2001MO-US009761.
 PF
 XX 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX (UNDE) UNIV DELAWARE.
 PA
 XX Kmiec EB, Gampier HB, Rice MC;
 PI WPI; 2001-639230/73.
 DR
 XX Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.
 XX
 PS Claim 7; Page 54; 294pp; English.
 XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APP), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolemia, thalassemia, sickle cell anemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SO Sequence 17 BP; 5 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 DB 2 ATGAACCGGAGG 13

RESULT 129
 ID ABA77317 standard; DNA; 17 BP.
 XX ABA77317;
 AC ABA77317;
 XX
 DT 24-JAN-2002 (first entry)
 XX

DE p53 mutation correcting oligonucleotide SEQ ID NO: 163.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 XX retinoblastoma; BRCA1, BRCA2; CPTA; cystic fibrosis; cancer; Factor V;
 KM cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1, HBA2;
 KM adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KM haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1, APOE;
 KM mismatch repair; MSH2, MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KM familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KM UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KM Alzheimer's disease; cytoskeletal; antickling; antianemic; haemostatic;
 KM antileptic; ss.

OS Homo sapiens.
 XX MO200173002-A2.
 PN 04-OCT-2001.
 PD 27-MAR-2001; 2001WO-US009761.
 PF 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.

XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.

XX Claim 7; Page 51; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CPTA, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention

SO Sequence 17 BP; 4 A; 6 C; 6 G; 1 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 16 ATGAACCGGAGG 27
 3 ATGAACCGGAGG 14

RESULT 130
 ABA77318/C
 ID ABA77318 standard; DNA; 17 BP.
 XX ABA77318;
 AC
 XX 24-JAN-2002 (first entry)

XX p53 mutation correcting oligonucleotide SEQ ID NO: 164.

XX Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KM retinoblastoma; BRCA1, BRCA2; CPTA; cystic fibrosis; cancer; Factor V;
 KM cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1, HBA2;
 KM adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KM haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1, APOE;
 KM mismatch repair; MSH2, MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KM familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KM UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KM Alzheimer's disease; cytoskeletal; antickling; antianemic; haemostatic;
 KM antileptic; ss.

OS Homo sapiens.
 XX MO200173002-A2.
 PN 04-OCT-2001.
 PD 27-MAR-2001; 2001WO-US009761.
 PF 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.

XX (UYDE) UNIV DELAWARE.
 PA Kmiec EB, Gamper HB, Rice MC;
 XX WPI; 2001-639230/73.
 DR Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.

XX Claim 7; Page 52; 294pp; English.

XX The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CPTA, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSEN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention

SO Sequence 17 BP; 1 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 12; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 16 ATGAACCGGAGG 27
 15 ATGAACCGGAGG 4

RESULT 131
 ABA77346/C
 ID ABA77346 standard; DNA; 17 BP.
 XX ABA77346;
 AC
 XX

DT 24-JAN-2002 (first entry)
 XX
 DE P53 mutation correcting oligonucleotide SEQ ID NO: 192.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; AFP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cyclostatic; antitickling; antianemic; haemostatic;
 KW antileptic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 01-UTN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.
 XX
 PI Kmiec EB, Gampier HB, Rice MC;
 XX
 DR WPI; 2001-639230/73.
 XX
 PT Oligonucleotide for targeted alterations of genetic sequences and for
 PT treating cystic fibrosis, comprises at least one mismatch and chemical
 PT modification.
 XX
 PS Claim 7; Page 54; 294pp; English.
 XX
 CC The present invention provides single-stranded oligonucleotides which can
 CC be used for the targeted alteration of genomic sequences, where the
 CC oligonucleotide has at least one mismatch compared with the genomic
 CC sequence to be altered. In particular, these sequences are directed at
 CC the following genes: adenosine deaminase, p53, beta-globin,
 CC retinoblastoma, BRCA1, BRCA2, CTR, cyclin-dependent kinase inhibitor 2A
 CC (CDKN2A), APC, Factor V, Factor VIII, Factor IX, haemoglobin alpha locus
 CC 1 (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6,
 CC apolipoprotein E (APOE), LDL receptor (LDLR), UDP-glucuronosyltransferase
 CC (UGT1), amyloid precursor protein (APC), presenilin-1 (PSEN1) and
 CC presenilin-2 (PSN2). These can be used in the gene therapy of diseases
 CC such as cancer, adenosine deaminase deficiency, cystic fibrosis,
 CC haemophilia, hypercholesterolaemia, thalassemia, sickle cell anaemia,
 CC Alzheimer's disease, melanoma, adenomatous polyposis of the colon and
 CC various syndromes. The present sequence is one of the gene correcting
 CC oligonucleotides of the invention
 XX
 SO Sequence 17 BP; 1 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 XX
 QY Query Match 2.0%; Score 12; DB 4; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Db Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 16 ATGAACCGAGG 27
 16 ATGAACCGAGG 5

XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMMP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7365.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMMP-1; hGDMMP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AECM-) AECOMICA INC.
 XX
 PI Gu Y, Yi Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMMP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMMP-1.
 XX
 PS Disclosure; SEQ ID NO 7365; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMMP-1). The protein and polynucleotide sequences of hGDMMP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMMP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMMP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMMP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMMP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMMP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMMP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionization, as
 CC therapeutic supplement in patients having specific deficiency in hGDMMP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMMP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMMP-1, in particular heart
 CC and skeletal muscle disorders. hGDMMP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMMP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SO Sequence 17 BP; 7 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 QY Query Match 2.0%; Score 12; DB 6; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
 |||||
 Db 5 GAAATTCAGTT 16

RESULT 133

ABN07376
 ID ABN07376 standard; DNA; 17 BP.
 XX
 AC ABN07376;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7367.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200192524-A2.
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0268660P.
 XX
 PA (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 7367; 214pp; English.
 XX
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionization, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.

CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX

SO Sequence 17 BP; 8 A; 1 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. NO. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 499 GAAATTCAGTT 510
 |||||
 Db 2 GAAATTCAGTT 13

RESULT 134

ABN07375
 ID ABN07375 standard; DNA; 17 BP.
 XX
 AC ABN07375;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7367.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200192524-A2.
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0268660P.
 XX
 PA (AEOM-) AEOMICA INC.
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 DR WPI; 2002-179446/23.
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 XX
 PS Disclosure; SEQ ID NO 7367; 214pp; English.
 XX
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1

PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMRP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMRP-1.
 XX
 PS Disclosure; SEQ ID NO 7364; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMRP-1). The protein and polynucleotide sequences of hGDMRP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMRP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMRP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMRP-1
 CC expressing the proteins. The hGDMRP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMRP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMRP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionization, as
 CC therapeutic supplement in patients having specific deficiency in hGDMRP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMRP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMRP-1, in particular heart
 CC and skeletal muscle disorders. hGDMRP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMRP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 7 A; 3 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 SQ Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 499 GAAATTCAGTT 510
 Db 6 GAAATTCAGTT 17
 XX
 RESULT 137
 ABN07374
 ID ABN07374 standard; DNA; 17 BP.
 XX
 AC ABN07374;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMRP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7366.
 XX
 KM Human; genome-derived myosin-like protein 1; GDMRP-1; heart;
 KM muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KM skeletal muscle disorder; amplicon; screening; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 30-JAN-2001; 2001WO-US000670.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 DR
 XX
 PT New polypeptide, for raising antibodies that recognize hGDMRP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMRP-1.
 XX
 PS Disclosure; SEQ ID NO 7366; 214pp; English.
 XX
 CC The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMRP-1). The protein and polynucleotide sequences of hGDMRP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMRP-1
 CC nucleic acids can be used as probes to detect, characterize and quantify
 CC hGDMRP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMRP-1
 CC expressing the proteins. The hGDMRP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMRP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMRP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption ionization, as
 CC therapeutic supplement in patients having specific deficiency in hGDMRP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMRP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMRP-1, in particular heart
 CC and skeletal muscle disorders. hGDMRP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMRP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 7 A; 2 C; 4 G; 4 T; 0 U; 0 Other;
 XX
 SQ Query Match 2.0%; Score 12; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 499 GAAATTCAGTT 510
 Db 4 GAAATTCAGTT 15
 XX
 RESULT 138
 ABV85812
 ID ABV85812 standard; DNA; 17 BP.
 XX
 AC ABV85812;
 XX
 DT 11-DEC-2002 (first entry)
 XX
 DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:805.
 XX
 KM Human; UDP-GalNAc:polypeptide N-acetylglactosaminyltransferase 10;
 KM pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
 KM

KV		ss.
XX	Homo sapiens.	
OS	Synthetic.	
XX		
PN	EP1243660-A2.	
XX		
PD	25-SEP--2002.	
XX		
PJ	25-JAN-2002; 2002EP-00001161.	
XX		
PR	30-JAN-2001; 2001WO-US000663.	
PT	30-JAN-2001; 2001WO-US000664.	
PR	30-JAN-2001; 2001MO-US000665.	
PR	30-JAN-2001; 2001MO-US000666.	
PR	30-JAN-2001; 2001MO-US000667.	
PR	30-JAN-2001; 2001MO-US000668.	
PR	30-JAN-2001; 2001MO-US000669.	
PR	30-JAN-2001; 2001MO-US000670.	
PR	23-MAY-2001; 2001US-00864761.	
PR	30-AUG-2001; 2001US-0315984P.	
PA	(AEOM-) AEOMICA INC.	
PI	Zhang J, Gu Y, Nguyen C;	
DH	WFI; 2002-724954/79.	
NL	Nucleic acid encoding human UDP-GalNAc:polypeptide N-	
cetylglucosaminyltransferase 10 protein is useful to diagnose, prevent		
treat disorders associated with reduced or over expression of the		
encoded protein.		
Example 2; SEQ ID NO 805; 59pp; English.		
The present invention describes an isolated nucleic acid (I) encoding a		
human UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 (pp-		
GalnTase 10, EC 2.4.1.41) protein. Human pp-galnTase 10 is located to		
chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the		
present invention can be used in therapy, particularly to prevent or		
treat a disorder associated with decreased expression or activity of pp-		
GalnTase. The sequences given in ABY85011 to ABY8689 and ABP3502 to		
ABP3504 are given in the exemplification of the present invention. N.B.		
The sequence data for this patent is not represented in the printed		
specification but is based on sequence information supplied by the		
European Patent Office		
Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;		
Query Match 2.0%; Score 12; DB 6; Length 17;		
Best Local Similarity 100.0%; Pred.No. 1.2e+05;		
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CY 165 CCAGCTGAATT 176 DB 5 CCACGTGAAAT 16		
RESULT 139		
ABY85811		
ID ABY85811 standard; DNA; 17 BP. XX XX AYB85811; DT 11-DEC-2002 (first entry) DE Human pp-galnTase 10 scanning 17-mer SEQ ID NO:804. KW Human; UDP-GalNac:polipeptide N-acetylgalectosaminyltransferase 10; SS pp-galnTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning; XX XX Homo sapiens. OS		

OS	Synthetic.
XX	
PN	EP1243660-A2.
XX	
PD	25-SEP-2002.
XX	
PF	25-JAN-2002; 2002EP-00001161.
XX	
PR	30-JAN-2001; 2001WO-US000663.
XX	
PR	30-JAN-2001; 2001WO-US000664.
XX	
PR	30-JAN-2001; 2001WO-US000665.
XX	
PR	30-JAN-2001; 2001WO-US000666.
XX	
PR	30-JAN-2001; 2001WO-US000667.
XX	
PR	30-JAN-2001; 2001WO-US000668.
XX	
PR	30-JAN-2001; 2001WO-US000669.
XX	
PR	30-JAN-2001; 2001WO-US000670.
XX	
PR	23-MAY-2001; 2001US-00864761.
XX	
PR	30-AUG-2001; 2001US-0315984P.
XX	
PA	(AECOM-) AECOMICA INC.
PI	
PI	Zhang J, Gu Y, Nguyen C;
XX	
DR	WPI: 2002-724954/79.
XX	
PT	Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT	cetylGalactosaminyltransferase 10 protein is useful to diagnose, prevent
PT	and treat disorders associated with reduced or over expression of the
XX	encoded protein.
XX	
XX	Example 2; SEQ ID NO 804; 59pp; English.
XX	
CC	The present invention describes an isolated nucleic acid (I) encoding a
CC	human UDP-GalNAc:polypeptide N-acetylGalactosaminyltransferase 10 (pp-
CC	GalNAcase 10, EC 2.4.1.41) protein. Human pp-GalNAc 10 is located to
CC	chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC	present invention can be used in therapy, particularly to prevent or
CC	treat a disorder associated with decreased expression or activity of pp-
CC	GalNAcase. The sequences given in ABV5011 to ABV6689 and ABP5302 to
CC	ABP53504 are given in the exemplification of the present invention. N.B.
CC	The sequence data for this patent is not represented in the printed
CC	specification but is based on sequence information supplied by the
CC	European Patent Office
XX	
XX	
SEQ	Sequence 17 BP; 4 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX	
Query Match	2.0%; Score 12; DB 6; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	165 CCACGTGAATT 176
Db	6 CCACGTGAATT 17
XX	
RESULT 140	
ABV85814	
ID	ABV85814 standard; DNA; 17 BP.
XX	
AC	ABV85814;
XX	
DT	11-DEC-2002 (first entry)
XX	
DE	Human pp-GalNAc 10 scanning 17-mer SEQ ID NO:807.
XX	
KW	Human; UDP-GalNAc:polypeptide N-acetylGalactosaminyltransferase 10;
KW	pp-GalNAcase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX	ss.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	EP1243660-A2

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XX 25-SEP-2002.
XX
XX 25-JAN-2002; 2002EP-00001161.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
XX PT cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX PT and treat disorders associated with reduced or over expression of the
XX PT encoded protein.
XX
XX Example 2; SEQ ID NO 807; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
XX CC human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX CC GANTase 10, EC 2.4.1.41) protein. Human pp-GANTase 10 is located to
XX CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX CC present invention can be used in therapy, particularly to prevent or
XX CC treat a disorder associated with decreased expression or activity of pp-
XX CC GANTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
XX CC ABP53504 are given in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent is not represented in the printed
XX CC specification but is based on sequence information supplied by the
XX CC European Patent Office
XX
XX SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 165 CCACGTGGAATT 176
XX 3 CCACGTGGAATT 14
XX
XX Db
XX
XX RESULT 141
XX ABV85815
XX ID ABV85815 standard; DNA; 17 BP.
XX
XX AC ABV85815;
XX
XX DT 11-DEC-2002 (first entry)
XX
XX DE Human pp-GANTase 10 scanning 17-mer SEQ ID NO:808.
XX
XX KW Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
XX KW pp-GANTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX KW ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN EP1243660-A2.
XX
XX PD 25-SEP-2002.
XX
XX

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PF 25-JAN-2002; 2002EP-00001161.
XX
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhang J, Gu Y, Nguyen C;
XX
XX WPI; 2002-724954/79.
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
XX PT cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX PT and treat disorders associated with reduced or over expression of the
XX PT encoded protein.
XX
XX Example 2; SEQ ID NO 808; 59pp; English.
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
XX CC human UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX CC GANTase 10, EC 2.4.1.41) protein. Human pp-GANTase 10 is located to
XX CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX CC present invention can be used in therapy, particularly to prevent or
XX CC treat a disorder associated with decreased expression or activity of pp-
XX CC GANTase. The sequences given in ABV85011 to ABV86689 and ABP53502 to
XX CC ABP53504 are given in the exemplification of the present invention. N.B.
XX CC The sequence data for this patent is not represented in the printed
XX CC specification but is based on sequence information supplied by the
XX CC European Patent Office
XX
XX SQ Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 165 CCACGTGGAATT 176
XX 2 CCACGTGGAATT 13
XX
XX Db
XX
XX RESULT 142
XX ABV85816
XX ID ABV85816 standard; DNA; 17 BP.
XX
XX AC ABV85816;
XX
XX DT 11-DEC-2002 (first entry)
XX
XX DE Human pp-GANTase 10 scanning 17-mer SEQ ID NO:809.
XX
XX KW Human; UDP-GalNAc:polypeptide N-acetylalactosaminyltransferase 10;
XX KW pp-GANTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX KW ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN EP1243660-A2.
XX
XX PD 25-SEP-2002.
XX
XX PF 25-JAN-2002; 2002EP-00001161.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX

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PR	30-JAN-2001;	2001WO-US000664.	
PR	30-JAN-2001;	2001WO-US000665.	
PR	30-JAN-2001;	2001WO-US000666.	
PR	30-JAN-2001;	2001WO-US000667.	
PR	30-JAN-2001;	2001WO-US000668.	
PR	30-JAN-2001;	2001WO-US000669.	
PR	30-JAN-2001;	2001WO-US000670.	
PR	23-MAY-2001;	2001US-00864761.	
PR	30-AUG-2001;	2001US-0315984P.	
XX			
PA	(AECOM-) AECOMICA INC.		
XX			
PI	Zhang J, Gu Y, Nguyen C;		
XX			
DR	WPI; 2002-724954/79.		
XX			
PT	Nucleic acid encoding human UDP-GalNAc:polypeptide N-		
PT	cetylglucosaminyltransferase 10 protein is useful to diagnose, prevent		
PT	and treat disorders associated with reduced or over expression of the		
PT	encoded protein.		
XX			
PS	Example 2; SEQ ID NO 809; 59pp; English.		
XX			
CC	The present invention describes an isolated nucleic acid (I) encoding a		
CC	human UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10 (p-		
CC	GalNAse 10; EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to		
CC	chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the		
CC	present invention can be used in therapy, particularly to prevent or		
CC	treat a disorder associated with decreased expression or activity of pp-		
CC	GaNTase. The sequences given in ABV85011 to ABV86689 and ABP33502 to		
CC	ABP33504 are given in the exemplification of the present invention. N.B.		
CC	The sequence data for this patent is not represented in the printed		
CC	specification but is based on sequence information supplied by the		
CC	European Patent Office		
XX			
SQ	Sequence 17 BF; 4 A; 6 C; 4 G; 3 T; 0 U; 0 Other;		
XX			
QY	Query Match	2.0%; Score 12; DB 6; Length 17;	
	Best Local Similarity	100.0%; Pred. No. 1.2e+05;	
	Matches 12; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
	165 CCACTGGAAAT 176		
	1 CCACTGGAAAT 12		
DB			
	RESULT 143		
ID	ABV85813 standard; DNA; 17 BP.		
XX			
AC	ABV85813;		
XX			
DT	11-DEC-2002 (first entry)		
XX			
DE	Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:806.		
XX			
KW	Human; UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10;		
KW	pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;		
XX	85.		
OS	Homo sapiens.		
XX			
OS	Synthetic.		
XX			
PN	EP1243660-A2.		
XX			
PD	25-SEP-2002.		
XX			
PF	25-JAN-2002; 2002EP-00001161.		
XX			
PR	30-JAN-2001; 2001WO-US000663.		
PR	30-JAN-2001; 2001WO-US000664.		
PR	30-JAN-2001; 2001WO-US000665.		
PR	30-JAN-2001; 2001WO-US000666.		

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PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 30-AUG-2001; 2001US-0315984P.
PA (ABOM-) AEOMICA INC.
PI Zhang J, Gu Y, Nguyen C;
XX WPI; 2002-724954/79.
DR
XX
XX
XX Nucleic acid encoding human UDP-GalNAc:polypeptide N-
PT cetylglucosaminyltransferase 10 protein is useful to diagnose, prevent
PT and treat disorders associated with reduced or over expression of the
PT encoded protein.
XX
XX
XX Example 2; SEQ ID NO 806; 59pp; English.
PS
XX
XX The present invention describes an isolated nucleic acid (I) encoding a
CC human UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 10 (pp-
CC GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
CC present invention can be used in therapy, particularly to prevent or
CC treat a disorder associated with decreased expression or activity of pp-
CC GaNTase. The sequences given in ABV65011 to ABV86689 and ABP53502 to
CC ABP53504 are given in the exemplification of the present invention. N.B.
CC The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied by the
CC European Patent Office
XX
XX
XX Sequence 17 BP; 4 A; 5 C; 4 G; 4 T; 0 U; 0 Other;
SQ
XX
XX
XX Query Match 2.0%; Score 12; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 165 CCACGTGAATT 176
DB 4 CCACGTGAATT 15
RESULT 144
ID ABV79548/C
XX ABV79548 standard; DNA; 17 BP.
AC
XX ABV79548;
AC
XX
XX 03-JAN-2003 (first entry)
DT
XX
XX Human HTP1 scanning oligonucleotide SEQ ID 794.
DE
XX
XX Human; gene therapy; tumour suppressor; HTP1; chromosome 10p12.1;
KM human testis expressed Patched like protein; testis; adrenal; liver;
KM male germ cell development; bone marrow; brain; kidney; lung; placenta;
KM prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI229046-A2.
PN
XX
XX 07-AUG-2002.
PD
XX
XX 28-JAN-2002; 2002EP-00001167.
PF
XX
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR

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PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 167; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 386 TGCACCGCGCGC 397
DB 17 TGCACCGCGCGC 6
RESULT 145
ABV79554/C
ID ABV79554 standard; DNA; 17 BP.
XX
XX ABV79554;
XX
XX 03-JAN-2003 (first entry)
XX
XX Human HTPL scanning oligonucleotide SEQ ID 800.
XX
XX Human; Gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX
XX Homo sapiens.
XX
XX EP1229046-A2.
XX
XX 07-AUG-2002.
XX
XX 28-JAN-2002; 2002EP-00001167.
XX
XX 30-JAN-2001; 2001MO-US000663.
XX
XX 30-JAN-2001; 2001MO-US000664.
XX
XX 30-JAN-2001; 2001MO-US000665.
XX
XX 30-JAN-2001; 2001MO-US000667.
XX
XX 30-JAN-2001; 2001MO-US000668.

```

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PR 30-JAN-2001; 2001MO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327898P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Zhan J;
XX
XX WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
XX Example 2; Page 168; 718pp; English.
XX
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and ABB98519 to ABB98520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 385 CTGCACCGCGCC 396
DB 12 CTGCACCGCGCC 1
RESULT 146
ACC53318
ID ACC53318 standard; DNA; 17 BP.
XX
XX ACC53318;
XX
XX 27-JUN-2003 (first entry)
XX
XX Human tumour suppressor sequence #2085.
XX
XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.
XX
XX Homo sapiens.
XX
XX FR2826373-A1.
XX
XX 27-DEC-2002.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX 20-JUN-2001; 2001FR-00008139.
XX
XX (MOLE-) MOLECULAR ENGINES LAB SA.
XX

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PI Tuijnder M, Telerman A, Amson R;
 DR WPI; 2003-250498/25.
 XX
 XX New nucleic acid sequences associated with tumor suppression, regression,
 PT apoptosis or virus resistance are useful to diagnose and treat viral
 PT disease, development of tumor cells and cell degeneration.
 XX
 PS Claim 1; Page 521; 798bp; French.
 XX
 CC This sequence represents an isolated nucleic acid sequence associated
 CC with tumor suppression or regression, apoptosis or virus resistance. The
 CC invention relates to these sequences or sequences having at least 80%
 CC identity to them, and polypeptides encoded by the sequences or
 CC polypeptides having 80% identity to the polypeptide sequences. The
 CC invention is used to diagnose or treat viral disease or disease
 CC characterized by development of tumour cells or cellular degeneration
 CC
 XX Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 2.0%; Score 12; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 355 CGCAGGCTGAG 366
 Db 4 CGCAGGCTGAG 15
 RESULT 147
 ABT37905
 ID ABT37905 standard; DNA; 17 BP.
 XX
 XX ABT37905;
 AC
 DT 12-UUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID No 3542.
 XX
 XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
 KM antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; protein chip; gene therapy; tumour suppression;
 KM human fukutin; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO2003025175-A2.
 PN
 PD 27-MAR-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004208.
 PF
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 ZA
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 XX New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 448; 720pp; French.
 XX
 CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,

identifying, quantifying and/or amplifying a nucleic acid, e.g., as one component of a gene chip, in vitro as (anti)sense reagents, and for production of recombinant polypeptides. Any of the nucleic acids, polypeptides, vectors containing the nucleic acids, cells containing the vector or antibodies directed against the polypeptides are useful for preparation of pharmaceuticals for prevention and/or treatment of viral diseases that are characterized by development of tumours or cell degeneration, specifically cancer but also Alzheimer's disease and schizophrenia. Analysis of the expression of the 17 mer nucleic acids in patient samples is useful for diagnosis and/or prognosis of these diseases. The polypeptides can also be used to generate antibodies, and both the polypeptide and antibodies are useful as components of protein chips. The nucleic acid sequences of the invention can be used in gene therapy. This polynucleotide sequence represents a tumour suppression related human fukutin oligonucleotide of the invention

Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match	2.0%; Score 12; DB 7; Length 17;
Best Local Similarity	100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

355 CGCAAGGCTGAG 366
|||||
4 CGCAAGGCTGAG 15

Db

RESULT 148
ABT36423/c
ID ABT36423 standard; DNA; 17 BP.
AC ABT36423;
XX
XX
DT 12-JUN-2003 (first entry)
XX
DE Tumour suppression related human fukutin oligo SEQ ID NO 2060.

Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip; antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease; schizophrenia; protein chip; gene therapy; tumour suppression; human fukutin; ds.

XX
XX Homo sapiens.
OS
XX
XX MO2003025175-A2.
PN
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002MO-IB004208.
XX
PR 17-SEP-2001; 2001FR-00011978.
PA (MOL-) MOLECULAR ENGINES LAB.
XX
PI Tejerman A, Amson R, Tuijinder M;
DR WPI; 2003-313353/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 273; 720pp; French.
XX

The invention relates to a novel isolated 17 mer nucleic acid sequence, given in the specification, a sequence containing at least 15 consecutive nucleotides from the 17 mer sequence, a sequence with, after optimal alignment, at least 80 % identity to the 17 mer sequence, a sequence that hybridizes to them under highly stringent conditions, or the complement of any of them, or the corresponding RNA. The novel isolated nucleic acids of the invention are useful as probes and primers for detecting, identifying, quantifying and/or amplifying a nucleic acid, e.g., as one component of a gene chip, in vitro as (anti)sense reagents, and for

CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the
 CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterized by development of tumors or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX
 SQ Sequence 17 BP; 4 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 313 AGCTGAGGATC 324
 Db 12 AGCTGAGGATC 1

RESULT 149
 ADBT34697
 ID ABT34697 standard; DNA; 17 BP.
 AC ABT34697;
 XX
 DT 12-JUN-2003 (first entry)
 XX
 DE Tumour suppression related human fukutin oligo SEQ ID NO 334.
 XX
 KM Cytostatic; vinicide; neuroprotective; nootropic; neuroleptic; gene chip;
 KM antiense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; protein chip; gene therapy; tumour suppression;
 KM human fukutin; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003025175-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB04208.
 XX
 PR 17-SEP-2001; 2001FR-00011978.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijinder M;
 XX
 DR WPI; 2003-313353/30.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 73; 720pp; French.

XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
 CC given in the specification, a sequence containing at least 15 consecutive
 CC nucleotides from the 17 mer sequence, a sequence with, after optimal
 CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
 CC hybridizes to them under highly stringent conditions, or the complement
 CC of any of them, or the corresponding RNA. The novel isolated nucleic
 CC acids of the invention are useful as probes and primers for detecting,
 CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
 CC component of a gene chip, in vitro as (anti)sense reagents, and for
 CC production of recombinant polypeptides. Any of the nucleic acids,
 CC polypeptides, vectors containing the nucleic acids, cells containing the

CC vector or antibodies directed against the polypeptides are useful for
 CC preparation of pharmaceuticals for prevention and/or treatment of viral
 CC diseases that are characterized by development of tumors or cell
 CC degeneration, specifically cancer but also Alzheimer's disease and
 CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
 CC patient samples is useful for diagnosis and/or prognosis of these
 CC diseases. The polypeptides can also be used to generate antibodies, and
 CC both the polypeptide and antibodies are useful as components of protein
 CC chips. The nucleic acid sequences of the invention can be used in gene
 CC therapy. This polynucleotide sequence represents a tumour suppression
 CC related human fukutin oligonucleotide of the invention

XX
 SQ Sequence 17 BP; 8 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 ACCATGAAAGAA 472
 Db 5 ACCATGAAAGAA 16

RESULT 150
 ADB03447/C
 ID ADB03447 standard; DNA; 17 BP.
 XX
 AC ADB03447;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human MDZ7 scanning oligonucleotide SEQ ID 4433.
 XX
 KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
 KM zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 6p21.3-22.1;
 KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
 KM developmental disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI281758-A2.
 XX
 PD 05-FEB-2003.
 XX
 PF 30-JUL-2002; 2002EP-00016874.
 XX
 PR 02-AUG-2001; 2001US-00922181.
 XX
 PA (AEOM-) AEOMICA INC.
 XX
 PI Shannon M, Gu Y, Nguyen C;
 XX
 DR WPI; 2003-423107/40.
 XX
 PT New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MDZ3,
 PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 4433; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
 CC encoded at chromosome 7q42.1; MDZ4 is encoded at chromosome 6p21.3-22.2,
 CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
 CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MDZ3,
 CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX

SO Sequence 17 BP, 1 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 365 AGCCCGAGGGGC 376
|||||

Db 12 AGCCCGAGGGGC 1

RESULT 151

ADA99804

ID ADA99804 standard; DNA; 17 BP.

XX ADA99804;

XX 20-NOV-2003 (first entry)

XX Human MD23 scanning oligonucleotide SEQ ID 793.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 793; 103bp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

XX acids and proteins are also useful for diagnosing or monitoring a disease

XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

XX acids can also be used as probes to detect and characterize gross

XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

XX useful in constructing microarrays for measuring gene expression. The

XX CC proteins are useful as therapeutic agents for gene therapy or as

XX vaccines. The present sequence was used to illustrate the invention.

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGGA 445
|||||

Db 6 TTACTGCTGGA 17

RESULT 152

ADA99805

ID ADA99805 standard; DNA; 17 BP.

XX ADA99805;

XX 20-NOV-2003 (first entry)

XX Human MD23 scanning oligonucleotide SEQ ID 794.

XX Cytostatic; immunostimulant; gene therapy; vaccine; human;

XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

XX developmental disorder; ss.

XX Homo sapiens.

XX EPI281758-A2.

XX 05-FEB-2003.

XX 30-JUL-2002; 2002EP-00016874.

XX 02-AUG-2001; 2001US-00922181.

XX (AEOM-) AEOMICA INC.

XX Shannon M, Gu Y, Nguyen C;

XX WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

XX manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27 or MD212, e.g. cancer.

XX Example 8; SEQ ID NO 794; 103bp; English.

XX The present invention relates to novel human zinc finger-containing

XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

XX or in manufacturing a medicament for treating or preventing a disorder

XX associated with decreased or increased expression or activity of MD23,

XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

XX acids and proteins are also useful for diagnosing or monitoring a disease

XX caused by altered expression of MD23, MD24, MD27, or MD212. The probes are

XX useful in constructing microarrays for measuring gene expression. The

XX CC proteins are useful as therapeutic agents for gene therapy or as

XX vaccines. The present sequence was used to illustrate the invention.

Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTACTGCTGGA 445
|||||

Db 5 TTACTGCTGGA 16

RESULT 153

```

ADA99323/c
ID ADA99323 standard; DNA; 17 BP.
XX
AC ADA99323;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 312.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EPI281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 312; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 3 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 247 TCCTGGAGCCCC 258
DB 17 TCCTGGAGCCCC 6

```

```

XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EPI281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
PS WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 795; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 434 TTTACTGCTGGA 445
DB 4 TTTACTGCTGGA 15

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RESULT 154
ADA99806
ID ADA99806 standard; DNA; 17 BP.
XX
AC ADA99806;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 795.

```

```

RESULT 155
ADB03443/c
ID ADB03443 standard; DNA; 17 BP.
XX
AC ADB03443;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 4429.
XX
KM Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
OS Homo sapiens.
XX

```



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PN  EPI281758-A2.
XX
PD  05-FEB-2003.
XX
PF  30-JUL-2002; 2002EP-00016874.
XX
PR  02-AUG-2001; 2001US-00922181.
XX
PA  (AEOM-) AEOMICA INC.
XX
PI  Shannon M, Gu Y, Nguyen C;
XX
DR  WPI; 2003-423107/40.
XX
PT  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder
PT  associated with decreased or increased expression or activity of MD23,
PT  MD24, MD27 or MD212, e.g. cancer.
XX
PS  Example 8; SEQ ID NO 4429; 103pp; English.
XX
CC  The present invention relates to novel human zinc finger-containing
CC  proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC  encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC  MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC  15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC  or in manufacturing a medicament for treating or preventing a disorder
CC  associated with decreased or increased expression or activity of MD23,
CC  MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC  acids and proteins are also useful for diagnosing or monitoring a disease
CC  caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC  acids can also be used as probes to detect and characterize gross
CC  alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC  useful in constructing microarrays for measuring gene expression. The
CC  proteins are useful as therapeutic agents for gene therapy or as
CC  vaccines. The present sequence was used to illustrate the invention.
XX
SQ  Sequence 17 BP; 0 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  365 AGCCCCAGGGGC 376
    |||||
DB  16 AGCCCCAGGGGC 5

```

```

PA  (AEOM-) AEOMICA INC.
XX
PI  Shannon M, Gu Y, Nguyen C;
XX
DR  WPI; 2003-423107/40.
XX
PT  New zinc finger-containing proteins and nucleic acids, useful in
PT  manufacturing a medicament for treating or preventing a disorder
PT  associated with decreased or increased expression or activity of MD23,
PT  MD24, MD27 or MD212, e.g. cancer.
XX
PS  Example 8; SEQ ID NO 4431; 103pp; English.
XX
CC  The present invention relates to novel human zinc finger-containing
CC  proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC  encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC  MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC  15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC  or in manufacturing a medicament for treating or preventing a disorder
CC  associated with decreased or increased expression or activity of MD23,
CC  MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC  acids and proteins are also useful for diagnosing or monitoring a disease
CC  caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC  acids can also be used as probes to detect and characterize gross
CC  alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC  useful in constructing microarrays for measuring gene expression. The
CC  proteins are useful as therapeutic agents for gene therapy or as
CC  vaccines. The present sequence was used to illustrate the invention.
XX
SQ  Sequence 17 BP; 0 A; 8 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match      2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY  365 AGCCCCAGGGGC 376
    |||||
DB  14 AGCCCCAGGGGC 3

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PT associated with decreased or increased expression or activity of MD23,
MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 443; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 365 AGCCGAGGGGC 376
Db 13 AGCCGAGGGGC 2
XX
RESULT 158
ADA99807
ID ADA99807 standard; DNA; 17 BP.
AC ADA99807;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 796.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EP1281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 796; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 4 C; 4 G; 7 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY 434 TTACTGCTCGA 445
Db 3 TTACTGCTCGA 14
XX
RESULT 159
ADA99809
ID ADA99809 standard; DNA; 17 BP.
AC ADA99809;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MD23 scanning oligonucleotide SEQ ID 798.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KM zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KM chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KM developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EP1281758-A2.
PN
XX 05-FEB-2003.
PD
XX 30-JUL-2002; 2002EP-00016874.
PF
XX 02-AUG-2001; 2001US-00922181.
PR
XX (AEOM-) AEOMICA INC.
PA
XX Shannon M, Gu Y, Nguyen C;
PI
XX WPI; 2003-423107/40.
DR
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 798; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross

CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 434 TTTACTGCTGGA 445
|||||
1 TTTACTGCTGGA 12

RESULT 160
ADB03442/C
ID ADB03442 standard; DNA; 17 BP.
XX
AC ADB03442;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ7 scanning oligonucleotide SEQ ID 4428.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
OS Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 4428; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
SQ Sequence 17 BP; 0 A; 9 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 365 AGCCCGAGGAGG 376
|||||
17 AGCCCGAGGAGG 6

RESULT 161
ADA99329/C
ID ADA99329 standard; DNA; 17 BP.
XX
AC ADA99329;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human MDZ3 scanning oligonucleotide SEQ ID 318.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
OS Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 318; 103bp; English.
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
XX encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
XX MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
XX 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MDZ3,
XX MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
XX alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
SQ Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 246 CTCCTGAGAGCC 257
|||||
12 CTCCTGAGAGCC 1

```

RESULT 162
ADB03444/C
ID ADB03444 standard; DNA; 17 BP.
XX
XX ADB03444;
XX
XX 20-NOV-2003 (first entry)
XX
DE Human MD27 scanning oligonucleotide SEQ ID 4430.
XX
KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (ABOM-) ABOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
DR WPI; 2003-423107/40.
XX
PT New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
PS Example 8; SEQ ID NO 4430; 103bp; English.
XX
CC The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 0 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 12; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
QY 365 AGCCCGAGGGGC 376
DB 15 AGCCCGAGGGGC 4
XX
RESULT 163
ADA99808
ID ADA99808 standard; DNA; 17 BP.
XX
XX ADA99808;
XX
XX 20-NOV-2003 (first entry)
XX

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DE Human MD23 scanning oligonucleotide SEQ ID 797.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX
XX Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 797; 103pp; English.
XX
XX
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX
XX Sequence 17 BP; 2 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 2.0%; Score 12; DB 7; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 434 TTACTGCTGGA 445
XX |||||
XX 2 TTACTGCTGGA 13
XX
XX
XX RESULT 164
XX ABZ61994/C
XX ID ABZ61994 standard; RNA; 17 BP.
XX
XX AC ABZ61994;
XX
XX DT 21-WAR-2003 (first entry)
XX
XX DE Human H-Ras DNAzyme target #785.
XX
XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX

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PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 126; 185pp; English.
XX
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
XX CC ribozymes of the invention
XX
SQ Sequence 17 BP; 2 A; 3 C; 8 G; 0 T; 4 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 303 CCCCAACTCAG 314
DB 15 CCCCAACTCAG 4

RESULT 165
ABZ61385
ID ABZ61385 standard; RNA; 17 BP.
XX
XX AC ABZ61385;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human H-Ras DNAzyme target #176.
XX
XX DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KM anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.

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XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 114; 185pp; English.
XX
XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ65520 - ABZ65524,
XX CC ABZ65530 - ABZ65585 represent substrate/target sequences for the human
XX CC ribozymes of the invention
XX
SQ Sequence 17 BP; 0 A; 4 C; 12 G; 0 T; 1 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 373 GGGCTCGGGCGG 384
DB 1 GGGCTCGGGCGG 12

RESULT 166
ABZ61383
ID ABZ61383 standard; RNA; 17 BP.
XX
XX AC ABZ61383;
XX
XX DT 21-MAR-2003 (first entry)
XX
XX DE Human H-Ras DNAzyme target #174.
XX
XX DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
XX KM anti-rheumatic; cancer; AIDS; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200297114-A2.
XX
XX PD 05-DEC-2002.
XX
XX PF 29-MAY-2002; 2002WO-US016840.
XX
XX PR 29-MAY-2001; 2001US-0294140P.
XX PR 06-JUN-2001; 2001US-0296249P.
XX PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
XX
XX PI Mcswigen J;
XX
XX DR WPI; 2003-140484/13.
XX
XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX PS Claim 58; Page 114; 185pp; English.

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CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention

XX
SQ Sequence 17 BP; 0 A; 5 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.2e+05;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 372 GGGGCTGCGGCG 383
Db 6 GGGGCTGCGGCG 17

RESULT 167
ABZ61791/C
ID ABZ61791 standard; RNA; 17 BP.
XX
AC ABZ61791;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNAzyme target #582.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 122; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human

CC ribozymes of the invention

XX
SQ Sequence 17 BP; 3 A; 3 C; 8 G; 0 T; 3 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 CTGTGCCGACCA 278
Db 12 CTGTGCCGACCA 1

RESULT 168
ABZ61790/C
ID ABZ61790 standard; RNA; 17 BP.
XX
AC ABZ61790;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human H-Ras DNAzyme target #581.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KM enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;
KM anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
DR WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 58; Page 122; 185pp; English.

CC The invention relates to a novel short interfering RNA (siRNA) nucleic acid molecule or an enzymatic nucleic acid molecule, that modulates expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras, human immunodeficiency virus (HIV) or a component of HIV. The nucleic acid molecule of the invention has cytosstatic, anti-HIV, and anti-rheumatic activity. The nucleic acid molecules are useful for reducing CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are also useful for treating breast, ovarian, colorectal, lung, prostate, CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human ribozymes of the invention

XX
SQ Sequence 17 BP; 3 A; 4 C; 6 G; 0 T; 4 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 267 CTGTGCCGACCA 278
Db 14 CTGTGCCGACCA 3

RESULT 169
 ACC64654
 ID ACC64654 standard; DNA; 17 BP.
 XX
 AC ACC64654;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1901.
 XX
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Teerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 253; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases
 CC that are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 5 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 75 TGAAGACTTACT 86
 DB 5 TGAAGACTTACT 16
 XX
 RESULT 170
 ACC65317
 ID ACC65317 standard; DNA; 17 BP.
 XX
 AC ACC65317;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2564.
 XX
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM

KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Teerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 330; 738pp; French.
 XX
 CC The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases
 CC that are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 2 A; 4 C; 5 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 7; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 CTGAGCTTGGT 141
 DB 6 CTGAGCTTGGT 17
 XX
 RESULT 171
 ACC64816/c
 ID ACC64816 standard; DNA; 17 BP.
 XX
 AC ACC64816;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2063.
 XX
 KM Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KM tumour suppression; tumour reversion; apoptosis; virus resistance;
 KM viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KM schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX

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XX  Teleman A, Amson R, Tuijnder M;
XX  WPI; 2003-333167/31.
XX
XX  New isolated nucleic acid, useful for treating viral diseases associated
XX  with tumors and cell degeneration, also related polypeptides, antibodies
XX  and transfected cells.
XX
XX  Disclosure; Page 272; 738pp; French.
XX
XX  The present invention relates to murine oligonucleotides (ACC62754-
XX  ACC68806), which are associated with tumour suppression, tumour
XX  reversal, apoptosis and virus resistance. The oligonucleotides are
XX  useful as (1) as probes and primers for detecting, identifying,
XX  quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX  gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX  recombinant polypeptides. The oligonucleotides are useful for preparation
XX  of pharmaceuticals for prevention and/or treatment of viral diseases that
XX  are characterised by development of tumours or cell degeneration,
XX  specifically cancer but also Alzheimer's disease and schizophrenia.
XX
XX  Sequence 17 BP; 2 A; 4 C; 3 G; 8 T; 0 U; 0 Other;
XX
XX  Query Match      2.0%; Score 12; DB 7; Length 17;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  457 GAAACCATGAA 468
XX  |||||
XX  17 GAAACCATGAA 6
XX
XX  RESULT 172
XX  ID ADB40734/c
XX  ID ADB40734 standard; DNA; 17 BP.
XX
XX  ADB40734;
XX
XX  18-DEC-2003 (revised)
XX  04-DEC-2003 (first entry)
XX
XX  Tumour suppression/reversion associated nucleotide #1057.
XX
XX  Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX  primer; probe; tumour suppression; tumour reversion; apoptosis;
XX  virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX  diagnosis.
XX
XX  Homo sapiens.
XX
XX  WO2003040369-A2.
XX
XX  15-MAY-2003.
XX
XX  17-SEP-2002; 2002WO-IB004219.
XX
XX  17-SEP-2001; 2001FR-00011981.
XX
XX  (MOLE-) MOLECULAR ENGINES LAB.
XX
XX  Teleman A, Amson R, Tuijnder M;
XX
XX  WPI; 2003-441574/41.
XX
XX  New nucleic acid encoding human prostate membrane-specific antigen,
XX  useful e.g. for treatment of tumors and viral infection, also related
XX  polypeptide and antibodies.
XX
XX  Disclosure; Page 155; 771pp; French.
XX
XX  The invention relates to the isolation of 6327 nucleotide sequences,
XX  fragments of at least 15 consecutive nucleotides of these nucleotides, a

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CC  sequence having at least 80% identity, after optimal alignment, with the
CC  nucleotides, a sequence that hybridizes under stringent conditions with
CC  the nucleotides, or the complement, or corresponding RNA, of the
CC  nucleotides. The nucleotides are used as probes or primers for detecting,
CC  identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC  sense and antisense sequences, of nucleotides involved in tumour
CC  suppression or reversion, apoptosis and or viral resistance, to produce
CC  recombinant polypeptides, and to prepare transgenic animals, as
CC  experimental models. The nucleotides (also vectors containing them and
CC  cells containing the vectors), the encoded polypeptides and antibodies
CC  (Ab) against the polypeptide are useful for prevention and/or treatment
CC  of viral infections or diseases characterized by development of tumours
CC  or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC  Analysis of the expression of the nucleotides can be used for diagnosis
CC  and/or prognosis of these diseases. The nucleotides and polypeptides can
CC  also be used to screen for their specific interactive molecules,
CC  potentially useful for treating diseases associated with abnormal
CC  expression of the nucleotides.
XX
XX  Sequence 17 BP; 5 A; 2 C; 3 G; 7 T; 0 U; 0 Other;
XX
XX  Query Match      2.0%; Score 12; DB 9; Length 17;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  500 AAATTCAGTTC 511
XX  |||||
XX  17 AAATTCAGTTC 6
XX
XX  RESULT 173
XX  ID ADB43195
XX  ID ADB43195 standard; DNA; 17 BP.
XX
XX  ADB43195;
XX
XX  18-DEC-2003 (revised)
XX  04-DEC-2003 (first entry)
XX
XX  Tumour suppression/reversion associated nucleotide #3518.
XX
XX  Cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
XX  primer; probe; tumour suppression; tumour reversion; apoptosis;
XX  virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
XX  diagnosis.
XX
XX  Homo sapiens.
XX
XX  WO2003040369-A2.
XX
XX  15-MAY-2003.
XX
XX  17-SEP-2002; 2002WO-IB004219.
XX
XX  17-SEP-2001; 2001FR-00011981.
XX
XX  (MOLE-) MOLECULAR ENGINES LAB.
XX
XX  Teleman A, Amson R, Tuijnder M;
XX
XX  WPI; 2003-441574/41.
XX
XX  New nucleic acid encoding human prostate membrane-specific antigen,
XX  useful e.g. for treatment of tumors and viral infection, also related
XX  polypeptide and antibodies.
XX
XX  Disclosure; Page 443; 771pp; French.
XX
XX  The invention relates to the isolation of 6327 nucleotide sequences,
XX  fragments of at least 15 consecutive nucleotides of these nucleotides, a
XX  sequence having at least 80% identity, after optimal alignment, with the
XX  nucleotides, a sequence that hybridizes under stringent conditions with
XX  the nucleotides, or the complement, or corresponding RNA, of the

```


CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, or nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

SQ Sequence 17 BP; 5 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGAG 366
 Db 4 CGCAGGCTGAG 15

RESULT 174
 ADB45286
 ID ADB45286 standard; DNA; 17 BP.
 XX ADB45286;
 AC 18-DEC-2003 (first entry)
 XX
 DT
 DE Tumour suppression/reversion associated nucleotide #5609.
 XX
 KW cytosolic; antiviral; neuroprotective; nocitropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN MO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-1B004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINEES LAB.
 XX
 PI Tejerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-441574/41.
 XX
 FT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 687; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce

CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

SQ Sequence 17 BP; 4 A; 3 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 9; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 355 CGCAGGCTGAG 366
 Db 4 CGCAGGCTGAG 15

RESULT 175
 AAQ06031/c
 ID AAQ06031 standard; DNA; 18 BP.
 XX
 AC AAQ06031;
 XX
 DT 17-DEC-2001 (revised)
 DT 08-MAR-1992 (first entry)
 XX
 DE Sequence of VPI (-) sense probe for nucleotides 2283-2301 of VPI amino
 DE terminal genome region.
 XX
 KW Detection; hepatitis A virus; viral protein 1; polymerase chain reaction;
 KW ss.
 XX
 OS Hepatitis A virus.
 XX
 PN USN7469143-N.
 XX
 PD 04-SEP-1990.
 XX
 PF 24-JAN-1990; 90US-00469143.
 XX
 PR 24-JAN-1990; 90US-00469143.
 XX
 PA (USSH) NAT INST OF HEALTH.
 PA (USDC) US SEC OF COMMERCE.
 XX
 DR WPI; 1990-304798/40.
 XX
 FT Detection of hepatitis A virus in samples - by extracting RNA,
 PT synthesizing cDNA, amplifying the cDNA by PCR and detecting amplified
 PT prod.
 XX
 PS Disclosure; Page 6; 28pp; English.

CC The labelled probes whose SOs are given in AAQ06030-2 are used for
 CC detecting amplified VPI amino terminal genome region HAV cDNA. The method
 CC of the invention provides a rapid, sensitive and specific test for
 CC detecting the presence of HAV in infected or contaminated samples of
 CC e.g., stools, serum, water or foodstuffs such as shellfish. (Note:
 CC Revised entry submitted to correct the patent number format of US
 CC Government-owned NITS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/nits_us.html.)
 XX
 SQ Sequence 18 BP; 4 A; 2 C; 3 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 AACCATGAAGA 471
 |||||
 16 AACCATGAAGA 5

RESULT 176
 AAQ26186/c
 ID AAQ26186 standard; DNA; 18 BP.

XX AAQ26186;
 AC
 XX 25-MAR-2003 (revised)
 DT 04-JAN-1993 (first entry)
 XX
 DE HLA-DR beta sub-type tailed probe DRB82 hybridising region.

XX Tissue typing; identity determination; disease susceptible; ss.

XX Synthetic.

XX WO9210589-A1.

XX 25-JUN-1992.

XX 06-DEC-1991; 91WO-US009294.

XX 06-DEC-1990; 90US-00623098.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;

XX Apple RJ;

XX WPI; 1992-234644/28.

PT Method for determining HLA-DR beta sub-type in DNA sample - comprises
 PT amplification and hybridisation with probes and primers, useful in tissue
 PT typing.

XX Example; Page 39; 90pp; English.

CC The sequence is that of the hybridising region of tailed probe DRB82 for
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
 CC sample. The method allows specific nucleic acid sequences of the second
 CC exon of HLA-DR beta genes to be amplified then probed for identification
 CC of polymorphic sequences. The amplified DNA is useful for typing
 CC homozygous or heterozygous samples from a variety of sources and for
 CC detecting allelic variants not distinguishable by serological methods.
 CC The typing system can be used in a reverse dot blot format which is
 CC simple and rapid to perform, produces detectable signals in minutes and
 CC can be utilised in tissue typing, determination of individual identity
 CC and identifying disease susceptible individuals. See also AAQ26092-
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 2 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255
 |||||
 17 ACCTCCTGGAGC 6

RESULT 177
 AAQ26149
 ID AAQ26149 standard; DNA; 18 BP.
 XX
 XX AAQ26149;

DT 25-MAR-2003 (revised)
 DT 04-JAN-1993 (first entry)

DE HLA-DR beta sub-type tailed probe DRB44 hybridising region.

XX Tissue typing; identity determination; disease susceptible; ss.

XX Synthetic.

XX WO9210589-A1.

XX 25-JUN-1992.

XX 06-DEC-1991; 91WO-US009294.

XX 06-DEC-1990; 90US-00623098.

XX (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX Erlich HA, Begovich AB, Bugawan T, Griffith RL, Scharf SJ;

XX Apple RJ;

XX WPI; 1992-234644/28.

PT Method for determining HLA-DR beta sub-type in DNA sample - comprises
 PT amplification and hybridisation with probes and primers, useful in tissue
 PT typing.

XX Example; Page 38; 90pp; English.

CC The sequence is that of the hybridising region of tailed probe DRB44 for
 CC use in a method for determining HLA-DR beta sub-type in a nucleic acid
 CC sample. The method allows specific nucleic acid sequences of the second
 CC exon of HLA-DR beta genes to be amplified then probed for identification
 CC of polymorphic sequences. The amplified DNA is useful for typing
 CC homozygous or heterozygous samples from a variety of sources and for
 CC detecting allelic variants not distinguishable by serological methods.
 CC The typing system can be used in a reverse dot blot format which is
 CC simple and rapid to perform, produces detectable signals in minutes and
 CC can be utilised in tissue typing, determination of individual identity
 CC and identifying disease susceptible individuals. See also AAQ26092-
 CC Q26367. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 18 BP; 3 A; 5 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 ACCTCCTGGAGC 255
 |||||
 2 ACCTCCTGGAGC 13

RESULT 178

AAQ38340
 ID AAQ38340 standard; DNA; 18 BP.

XX AAQ38340;

XX 25-MAR-2003 (revised)

DT 15-JUN-1993 (first entry)

DE EcoRI primer 3 for SRPA of corn DNA with multiple restriction enzymes.

XX Restriction fragment; PCR; RFLP; forensic typing; Zee mays; ss; labeled;

XX selective restriction fragment amplification.

XX Synthetic.

XX BP534858-A1.
 XX 31-MAR-1993.

```

XX 24-SEP-1992; 92EP-00402629.
XX 24-SEP-1991; 91EP-00402542.
XX (KEYG-) KEYGENE NV.
XX Zabeau M, Vos P;
XX WPI; 1993-102942/13.
XX
XX Selective controlled restriction fragment amplification of DNA - used for
XX gene analysis e.g. DNA fingerprinting, restriction fragment length
XX polymorphisms, etc.
XX
XX Example 4; Page 18; 43pp; English.
XX
XX The DNA from two corn inbred lines was restricted with TaqI and one of
XX AseI, PstI, EcoRI or Sse8387-I and tagged with the appropriate adaptors.
XX This DNA was used as template in PCR reactions using one of the labelled
XX TaqI primers, 1-4 and one of PstI-primers 1-4, AseI- primers 1-4, EcoRI-
XX primers 1-4 or Sse8387-I-primers 1-4, each primer confg. three selective
XX nucleotides at the 3' end. A total of 128 PCRs was performed and the
XX reaction prods. analysed. All primer combinations gave DNA fingerprints
XX of 50-100 bands per lane, except for the combination SseI/TaqI, which
XX gave only 10-15 bands per lane. The method can be used to identify
XX preselected DNA fragments which can be polymorphic, i.e. RFLPs. It is a
XX superior method for multiplex PCR. The method may also be used to detect
XX similarities between plant or animal varieties, species etc, or for
XX evaluating genetic distances and characterising the plant. See also
XX AAQ38313-43 and AAQ38907-16. (Updated on 25-MAR-2003 to correct PN
XX field.)
XX
XX Sequence 18 BP; 5 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 36 TTACCAATTCAA 47
XX |||||||||
XX Db 6 TTACCAATTCAA 17
XX
XX RESULT 179
XX AAQ34757 standard; DNA; 18 BP.
XX
XX AC AAQ34757;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-JUN-1993 (first entry)
XX
XX DE Activator oligonucleotide probe p53(A).
XX
XX KM Human; p53; anti-oncogene; assay; ss.
XX
XX OS Synthetic;
XX
XX PN WO9301313-A1.
XX
XX PD 21-JAN-1993.
XX
XX PF 06-JUL-1992; 92WO-GB001225.
XX
XX PR 05-JUL-1991; 91GB-00014525.
XX
XX PA (CYTO-) CYTOCELL LTD.
XX
XX PI Cardy DLM, Delnatte SYJ;
XX
XX DR WPI; 1993-045514/05.
XX

```

```

PT Homogeneous assay for nucleic acid sequences - obtd. by modulating enzyme
PT activity, by hybridisation of derived nucleic acid probes.
XX
XX Example 2; Page 27; 51pp; English.
XX
XX The activator oligonucleotide probe p53(A) may be used in an assay for
XX the detection of the human p53 anti-oncogene in human DNA. See also
XX AAQ34750-62. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 4 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 ATGAACCGGAGG 27
XX |||||||||
XX Db 4 ATGAACCGGAGG 15
XX
XX RESULT 180
XX AAQ34759/c
XX ID AAQ34759 standard; DNA; 18 BP.
XX
XX AC AAQ34759;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-JUN-1993 (first entry)
XX
XX DE Blocker oligonucleotide p53(B).
XX
XX KM Human; p53; anti-oncogene; assay; ss.
XX
XX OS Synthetic.
XX
XX PN WO9301313-A1.
XX
XX PD 21-JAN-1993.
XX
XX PF 06-JUL-1992; 92WO-GB001225.
XX
XX PR 05-JUL-1991; 91GB-00014525.
XX
XX PA (CYTO-) CYTOCELL LTD.
XX
XX PI Cardy DLM, Delnatte SYJ;
XX
XX DR WPI; 1993-045514/05.
XX
XX PT Homogeneous assay for nucleic acid sequences - obtd. by modulating enzyme
XX activity, by hybridisation of derived nucleic acid probes.
XX
XX Example 2; Page 27; 51pp; English.
XX
XX The blocker oligonucleotide p53(B) is complementary to its corresp.
XX activator probe p53(A). The oligonucleotide was synthesised with a 5'
XX bromodeoxyuridine nucleotide and may be used in an assay for the
XX detection of the human p53 anti-oncogene in human DNA. See also AAQ34750-
XX 62. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 18 BP; 1 A; 7 C; 6 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 ATGAACCGGAGG 27
XX |||||||||
XX Db 15 ATGAACCGGAGG 4
XX
XX RESULT 181
XX AAV39342/c
XX

```

ID AAV39342 standard; cDNA, 18 BP.
 XX AAV39342;
 AC
 XX
 XX
 DT 16-SEP-1998 (first entry)
 XX
 DE Human RAD54 mutation detecting PCR primer SEQ ID NO:50.
 XX
 XX Human; RAD54; cancer; xeroderma pigmentosum; Bloom syndrome;
 KM Werner's syndrome; ATR-X; diagnosis; detection; SNF2 superfamily;
 KM X-linked mental retardation with alpha-thalassemia syndrome; tumour;
 KM gene therapy; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX EP844305-A2.
 PN 27-MAY-1998.
 PD
 XX
 XX 10-NOV-1997; 97EP-00308998.
 PE
 XX 13-NOV-1996; 96US-0030676P.
 PR
 XX (SMK) SMITHKLINE BEECHAM CORP.
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Croce CM, Fishel RA, Rasio D, Robbins DJ;
 DR WPI; 1996-274189/25.
 XX
 XX Human hRAD54 DNA and polypeptide - and agonists, antibodies, antagonists,
 PT etc.
 PS
 XX Claim 18; Page 50; 64pp; English.
 XX
 CC The present sequence represents a PCR primer for use in a method of the
 CC invention for determining the genetic predisposition to cancer in an
 CC individual by detecting hRAD54 mutations in a sample. hRAD54 is a gene
 CC thought to be present in tumours that display allelic imbalance at 1p32,
 CC the chromosome 1 deletion in breast carcinomas. hRAD54 is useful for
 CC production of proteins, inter alia, that have been identified as novel
 CC hRAD54 by homology between the amino acid sequence given in AA62186 and
 CC known amino acid sequences such as yeast RAD54. hRAD54 proteins are used
 CC in the treatment of cancer, including Xeroderma Pigmentosum and Bloom
 CC syndrome, Werner's syndrome and X-linked mental retardation with alpha-
 CC thalassemia syndrome and breast cancer. hRAD54 polynucleotides are also
 CC useful for detecting complementary nucleotides for use as a diagnostic
 CC agent, especially useful for diagnosis of disease or susceptibility to
 CC diseases. hRAD54 polynucleotide, proteins, agonists and antagonists which
 CC are proteins are useful in gene therapy
 CC
 XX
 SQ Sequence 18 BP; 3 A; 5 C; 4 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 487 GAAGGCTGCAT 498
 DB 12 GAAGGCTGCAT 1
 XX
 RESULT 182
 ID AA221414 standard; DNA; 18 BP.
 XX AA221414;
 AC
 XX
 XX 02-DEC-1999 (first entry)
 DT
 XX Human MEK2 antisense oligonucleotide SEQ ID NO:17.
 DE

XX
 XX Human; MEK2; MAP kinase; MAPK/ERK kinase; erk activator kinase;
 KM mitogen activated protein kinase; expression; modulation; antisense;
 KM diagnosis; hepatocellular carcinoma; breast cancer; proliferation;
 KM differentiation; development; detection; probe; primer; tumour;
 KM phosphorothioate; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX 28-SEP-1999.
 PD
 XX 20-NOV-1998; 98US-00197378.
 PE
 XX 20-NOV-1998; 98US-00197378.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 PI Monia BP, Cowsett LM;
 DR WPI; 1999-561077/47.
 XX
 XX Antisense oligonucleotides of the MEK2 kinase gene, useful in diagnostic
 PT protocols in vitro and for inhibiting the expression of MEK2 in vivo for
 PT the treatment of human hepatocellular carcinomas and breast carcinomas.
 XX
 XX Claim 11; Col 39; 32pp; English.
 PS
 XX
 CC The present invention describes antisense oligonucleotides (asMEK2) of
 CC the human MEK2 dual specificity kinase gene. The MEK2 gene (also called
 CC MAPK2, mpk2, MAPK/ERK kinase 2, pmrk2 and erk activator kinase)
 CC represents a convergent target for the regulation of a range of cellular
 CC processes including proliferation, differentiation and development.
 CC asMEK2 may be used to inhibit the expression of MEK2 genes in vivo and/or
 CC in vitro. MEK2 has been shown to be over expressed in some tumour cells.
 CC Therefore, asMEK2 may be administered to a patient to treat
 CC hepatocellular carcinomas and breast carcinomas. asMEK2 may also be used
 CC as a diagnostic tool to specifically inhibit the expression of MEK2
 CC genes. The role of the inhibited genes in cellular pathways may then be
 CC evaluated. They may also be used as probes to detect sequences encoding
 CC MEK2 or as primers for the amplification of those sequences. AA21406 to
 CC AA22143 represent specifically claimed asMEK2's from the present
 CC invention
 CC
 XX
 SQ Sequence 18 BP; 1 A; 3 C; 7 G; 7 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 CTGACTTTGGT 141
 DB 6 CTGACTTTGGT 17
 XX
 RESULT 183
 ID AA231807 standard; DNA; 18 BP.
 XX AA231807;
 AC
 XX
 XX 24-JAN-2000 (first entry)
 DT
 XX Human G-alpha-13 antisense inhibitor ISIS# 20756.
 DE
 XX G-alpha-13; human; inhibitor; cancer; antisense compound; therapy; ss.
 KM
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX US5981732-A.
 PN

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XX 09-NOV-1999.
PD 04-DEC-1998; 98US-00205860.
PF 04-DEC-1998; 98US-00205860.
PR 04-DEC-1998; 98US-00205860.
PS (ISIS-) ISIS PHARM INC.
PI Cowser LM;
XX WPI; 1999-633376/54.
XX Antisense compound inhibiting expression of human G-alpha-13.
XX Claim 11; Col 39; 38pp; English.
XX This sequence represents an antisense inhibitor of the invention, and
XX inhibits the expression of the human G-alpha-13 protein. The antisense
XX compounds of the invention are of 8 to 30 nucleobases in length, that
XX inhibits the expression of the human G-alpha-13. The antisense compound
XX is useful for treating an animal, particularly humans, having or being
XX prone to a disease or condition associated with the expression of G-alpha
XX -13, such as cancer
SQ Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 AGGATCTTCACC 330
   |||||
   7 AGGATCTTCACC 18
Db

RESULT 184
ID AAAS2916
XX AAAS2916 standard; DNA; 18 BP.
AC AAAS2916;
XX
XX 20-BP-2000 (first entry)
DE Escherichia coli 055:H7 gnd gene PCR primer #8.
XX
XX Escherichia coli 055:H7; gnd; 6-phosphogluconate dehydrogenase; 6-PGD;
XX gastrointestinal infection; pathogen; 0157 lipopolysaccharide;
XX haemolytic uraemic syndrome; HUS; haemolytic anaemia; thrombocytopenia;
XX acute renal failure; polymorphism; PCR primer; ss.
XX
XX Escherichia coli.
OS
XX WO2000034484-A1.
XX
XX 15-JUN-2000.
XX
XX 08-DEC-1999; 99WO-US029149.
XX
XX 08-DEC-1998; 98US-011493P.
XX
XX (CHIL-) CHILDREN'S HOSPITAL & REGIONAL MEDICAL.
XX
XX Tarr PI;
XX
XX WPI; 2000-431304/37.
XX
XX New polynucleotide from Escherichia coli encoding 6-phosphogluconate
XX dehydrogenase and polymeric sequences in the nucleotide for detecting
XX strains of E. coli for diagnosis and food screening.
XX
XX Disclosure; Page 8; 84pp; English.

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CC The present sequence is a PCR primer used to amplify DNA beyond the 5'
CC and 3' termini of the E. coli 055:H7 gnd gene from total genomic DNA of
CC E. coli 055:H7 strain. The resulting sequence data was used to design a
CC primer pair to amplify the E. coli 055 and allele. The gnd gene, which
CC encodes 6-phosphogluconate dehydrogenase (6-PGD), has been studied in
CC fourteen strains of E. coli. Several polymorphisms have been found that
CC can be used to identify the presence of a particular strain of E. coli
CC and/or to differentiate one strain from another. A substitution of an
CC isoleucine molecule for a threonine molecule at amino acid position 218
CC can be used to differentiate highly pathogenic strains of 0157:H7 and
CC 055:H7 from less pathogenic strains of 0157:H7. E. coli 0157:H7 is an
CC extremely virulent food-borne, human pathogen that causes a spectrum of
CC diseases, including mild diarrhoea and the potentially lethal haemolytic
CC uraemic syndrome (HUS), which is defined as a triad of non-immune
CC microangiopathic haemolytic anaemia, thrombocytopenia, and acute renal
CC failure. The detection of one or more polymorphisms in 6-PGD can be used
CC to diagnose disease and to test for food or water contamination
XX
SQ Sequence 18 BP; 2 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 CCGCTACATCTC 197
   |||||
   4 CCGCTACATCTC 15
Db

RESULT 185
ID AA257673
XX AA257673 standard; DNA; 18 BP.
AC AA257673;
XX
XX 05-APR-2000 (first entry)
DE Human G-alpha-12 antisense inhibitor ISIS# 20661.
XX
XX G-alpha-12 inhibitor; antisense compound; cell differentiation; cancer;
XX cell growth; metastatic growth; ss; ISIS# 20661.
XX
XX Homo sapiens.
OS
XX US5998206-A.
XX
XX 07-DEC-1999.
XX
XX 23-FEB-1999; 99US-00256496.
XX
XX 23-FEB-1999; 99US-00256496.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Cowser LM;
XX
XX WPI; 2000-095920/08.
XX
XX Antisense inhibition of human G-alpha-12 expression.
XX
XX Example 15; Col 36; 36pp; English.
XX
XX This is a human G-alpha-12 antisense nucleotide sequence. G-alpha-12 is a
XX member of the G12/13 subfamily of G-proteins. The primary function of G-
XX alpha-12 is in cell differentiation and growth. The invention relates to
XX antisense compounds which are 8-30 nucleotides long (see AA257668-
XX 257746). The antisense molecules are targeted to the human G-alpha-12
XX nucleic acid molecule, and inhibit the expression of G-alpha-12. The
XX molecules preferably have a modified internucleotide linkage, and at
XX least one modified sugar moiety. The compounds target different regions
XX of the human G-alpha-12 RNA. The expression of human G-alpha 12 is
XX inhibited by contacting human cells or tissues in vitro with the
XX antisense molecules. The oligonucleotides are used in modulating the

```

CC function of nucleic acid molecules encoding G-alpha-12, ultimately
 CC modulating the amount of G-alpha-12 produced. The antisense compounds can
 CC be utilized for diagnostics, therapeutics, prophylaxis and as research
 CC agents and kits. They may be useful in the treatment of cancer, and
 CC metastatic growth

XX Sequence 18 BP; 4 A; 6 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 319 AGGATCTTCACC 330
 |||||
 Db 3 AGGATCTTCACC 14

RESULT 186
 AAZ44508

ID AAZ44508 standard; DNA; 18 BP.

XX AAZ44508;

AC 06-AUG-2003 (revised)
 DT 07-APR-2000 (first entry)

XX Z. mais restriction fragment amplification EcoRI-primer-3.

XX Detection; forensic; restriction fragment polymorphism; multiplex PCR;
 KM corn; primer; ss.

XX Zea mays.

OS

PN EP969102-A2.

XX 05-JAN-2000.

PF 24-SEP-1992; 99EP-00115309.

PR 24-SEP-1991; 91EP-00402542.

PR 24-SEP-1992; 92EP-00402629.

PA (KEYG-) KEYGENE NV.

PI Zabeau M, Vos P;

DR WPI; 2000-099430/09.

XX New oligonucleotides, useful for tagging restriction fragments for
 PT genetic diagnosis.

XX Example 4; Page 18; 42pp; English.

XX This invention describes a novel oligonucleotide (I) comprising an
 CC adapter sequence and part of the target sequence of a restriction
 CC endonuclease, and which has 1-10 selected nucleotides immediately
 CC adjacent to the 3' end of the target sequence. The products of the
 CC invention are used to tag restriction fragments which are to be amplified
 CC by the polymerase chain reaction (PCR). This technique may be used in the
 CC detection of restriction fragment polymorphisms (RFPs), including length
 CC polymorphisms. The products can also be used for genetic analysis, such
 CC as for the forensic typing of humans and the detection of the inheritance
 CC of determined traits in animals or plants and to monitor several diseases
 CC at once. The oligonucleotides and kits may also be used to identify
 CC species, races or varieties of animals or plants. The new adapters,
 CC oligonucleotides and methods for using them are more sensitive for
 CC detecting restriction fragment polymorphisms because not only differences
 CC in the target sites of the restriction endonuclease are detected as with
 CC prior art methods and oligonucleotides but also differences in the
 CC adjacent nucleotide sequences within the selective PCR primers. Multiplex
 CC PCR may only be used to monitor 5-8 different traits simultaneously and
 CC compromise conditions have to be established to allow all primer pairs to
 CC yield detectable products. In addition there are strong differences in

CC the efficiency of amplification of different fragments and products of
 CC certain primer pairs are not detectable with multiplex PCR. In contrast,
 CC using the new techniques, all the primers have a substantial part of
 CC their nucleotide sequence in common and by selecting Amplified Fragment
 CC Length Polymorphisms, the DNA markers are amplified with equal
 CC efficiency. AAZ44475-244526 represent primers used to illustrate the
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)
 XX

Qy Sequence 18 BP; 5 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 TTACCAATTCAA 47
 |||||
 Db 6 TTACCAATTCAA 17

RESULT 187
 ABA92907

ID ABA92907 standard; DNA; 18 BP.

XX ABA92907;

AC 08-APR-2002 (first entry)

DT Angiogenin inhibitor related oligonucleotide.

XX Angiogenin inhibitor; angiogenesis; ss.

XX Synthetic.

OS

PN KR99021167-A.

XX 25-MAR-1999.

PF 30-AUG-1997; 97KR-00044679.

PR 30-AUG-1997; 97KR-00044679.

PR (GREG) KOREA GREEN CROSS CORP.

PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.

PI Chae CB, Koh YS, Lee JE, Oh GS, Bae DG;

DR WPI; 2000-254109/22.

XX Angiogenin inhibitor.

XX Example 2; Page 6; 16pp; Korean.

XX The present invention describes angiogenin inhibitors. Angiogenin
 CC inhibitors can be used in the treatment of angiogenesis. The present
 CC sequence represents an oligonucleotide which is used in the
 CC exemplification of the present invention

XX Sequence 18 BP; 2 A; 2 C; 5 G; 9 T; 0 U; 0 Other;

Qy Query Match 2.0%; Score 12; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 547 CTGTATGAGTT 558
 |||||
 Db 2 CTGTATGAGTT 13

RESULT 188

AAAC6835

AC AAC66835;

XX XX 27-FEB-2001 (first entry)
XX XX
DE Human tankyrase II PCR primer g11-5'.
XX XX
KW Human; tankyrase II; telomere length; signal transduction; PCR primer;
KV ss.
XX Homo sapiens.
OS
XX WO200061813-A1.
PN
XX 19-OCT-2000.
PD
XX 10-APR-2000; 2000WO-US009558.
FF
XX 09-APR-1999; 99US-0128577P.
PR 13-APR-1999; 99US-0129123P.
XX (GERO-) GERON CORP.
PA
XX Morin GB, Funk WD, Piatydzek MA;
PI WPI: 2000-679503/66.
DR
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide encoding
PT the polypeptide useful for modulating or maintaining telomere length,
PR replicative capacity, apoptosis, chromosome packing or gene expression.
XX
PS Disclosure; Page 9; 52pp; English.
XX
CC The present invention relates to the isolation of the protein and coding
CC sequences of human tankyrase II. The tankyrase II protein is thought to
CC be involved in signal transduction in the cell, and to have binding
CC activity for other telomere-associated proteins. It is possible that it
CC plays a role in the regulation of telomere length, thus affecting the
CC replicative ability of the cell. The protein is useful for ribosylating
CC target proteins, for determining tankyrase II binding activity in a
CC sample, and for modulating telomere length in a cell. The present
CC sequence is a PCR primer used in the isolation of the tankyrase II coding
CC sequence
SQ Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 3; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CY 246 CTCCTGGAGCCC 257
DB 3 CTCCTGGAGCCC 14
RESULT 189
AAH47521
ID AAH47521 standard; DNA; 18 BP.
XX AAH47521;
XX
XX 30-NOV-2001 (first entry)
XX
XX Human MMP-8 cDNA amplifying sense primer E.
XX
XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
KW anti-arthritis; cytosolic; anti-Parkinsonian; neuroprotective;
KW neurotropic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; human; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX US1573-H.
PN
XX 03-JUL-2001.

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XX      22-OCT-1998;       98US-00178002.  
PF  
XX      22-OCT-1998;       98US-00178002.  
FR  
XX      (NOVS ) NOVARTIS AG.  
PA  
XX  
PI      Hu S;  
DR      WPI; 2001-431511/46.  
XX  
XX      New MMP-8alt polynucleotides and polypeptides useful as research reagents  
PT and materials for discovering treatments and diagnostics to human  
PT disease, or as targets for identifying inhibitors of MMP-8alt expression.  
XX  
XX      Example 1; Col 25; 25pp; English.  
PS  
CC      The invention relates to human MMP-8alt polypeptide and polynucleotides.  
CC      MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)  
CC CDNA. The MMP-8alt polypeptide can be expressed by standard recombinant  
CC methodology. The polynucleotides and polypeptides may be used as research  
CC reagents and materials for the discovery of treatments and diagnostics to  
CC human disease, and as targets for identifying modulators. Inhibitors of  
CC MMP-8alt polynucleotide or polypeptide expression may be used to treat  
CC and/or prevent arthritis, cancer and cancer metastasis, and diseases  
CC caused by cellular apoptosis including Parkinson's disease, Alzheimer's  
CC disease and Huntington's disease. Sequences AAH47517-21 represent PCR  
CC primers for cDNA and genomic DNA cloning of MMP-8alt  
SQ  
  
SQ      Sequence 18 BP; 7 A; 2 C; 6 G; 3 T; 0 U; 0 Other;  
  
Query Match          2.0%; Score 12; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
CY      94 GTACTGAGAGC 105  
        |||||  
DB      6 GTAGTGAGAAGC 17  
  
RESULT 190  
AAC99241  
ID      AAC99241 standard; DNA; 18 BP.  
XX  
XX      AAC99241;  
AC  
XX  
DT      06-MAR-2001 (first entry)  
XX  
DE      Probe sequence used in probe array SEQ ID 1.  
XX  
KW      Probe; probe array; probe-combined substrate; detection; ss.  
XX  
OS      Synthetic.  
CS  
PN      JF2000270896-A.  
PD  
XX      03-OCT-2000.  
PD  
XX      28-JAN-1999;   99JP-00019915.  
PF  
XX      28-JAN-1999;   99JP-00019915.  
PR  
XX      (CANO ) CANON KK.  
PA  
XX      WPI; 2001-027424/04.  
DR  
XX  
XX      A preparation of a probe-combined substrate, a probe array, detection of  
PT a target substance, specification of the base sequence of a single-  
PT stranded nucleic acid in a sample, and determination of a target  
PT substance in a sample.  
XX  
XX      Example 3; Page 11; 20pp; Japanese.
```

CC This invention relates to a probe-combined substrate, a probe array, and
 CC a method for the detection of a target substance in a sample. The probe
 CC array can be used for detecting a target substance with high reliability.
 CC Sequences AAC99241 - AAC99305 represent probes used in an array in an
 CC example illustrating the invention

XX Sequence 18 BP, 5 A, 6 C, 5 G, 2 T, 0 U, 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 DB 1 ATGAACCGGAGG 12

RESULT 191

AAC99283/c
 ID AAC99283 standard; DNA; 18 BP.

XX AAC99283;

DT 06-MAR-2001 (first entry)

DE Probe sequence used in probe array SEQ ID 43.

KM Probe; probe array; probe-combined substrate; detection; ss.

XX Synthetic.

XX JP2000270836-A.

XX 03-OCT-2000.

XX 28-JAN-1999; 99UP-00019915.

XX 28-JAN-1999; 99UP-00019915.

XX (CANO) CANON KK.

DR WPI; 2001-027424/04.

PT A preparation of a probe-combined substrate, a probe array, detection of

PT a target substance, specification of the base sequence of a single-

PT stranded nucleic acid in a sample, and determination of a target

XX substance in a sample.

XX Example 3; Page 17; 20pp; Japanese.

CC This invention relates to a probe-combined substrate, a probe array, and

CC a method for the detection of a target substance in a sample. The probe

CC array can be used for detecting a target substance with high reliability.

CC Sequences AAC99241 - AAC99305 represent probes used in an array in an

CC example illustrating the invention

QY 16 ATGAACCGGAGG 27
 |||||
 DB 18 ATGAACCGGAGG 7

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 DB 18 ATGAACCGGAGG 7

RESULT 192

AAC91122
 ID AAC91122 standard; DNA; 18 BP.

DT 20-MAR-2001 (first entry)

XX Fungal pathogenic species identification probe #8.

DE Fungal pathogenic; Internal Transcribed Spacer; ITS;

KM Opportunistic infection; ss.

XX Unidentified.

XX WO20007349-A2.

XX 07-DEC-2000.

XX 24-MAY-2000; 2000WO-EP004714.

XX 28-MAY-1999; 99EP-00870109.

XX 11-JUN-1999; 99US-0138621P.

XX (INNO-) INNOGENETICS NV.

XX (IRBI-) ENTERPRISE IRELAND T/A BIORESEARCH IRELA.

XX Smith T, Maher M, Martin C, James G, Rossau R, Van Der Weide M;

XX WPI; 2001-061555/07.

XX Detecting and identifying fungal pathogens, especially *Candida*,

XX *Cryptococcus* and *Aspergillus*, comprises hybridizing the amplified nucleic

XX acid of the fungal pathogen with a probe from the internal transcribed

XX spacer region of a DNA.

XX Claim 1; Page 46; 59pp; English.

XX The present invention relates to detecting and identifying fungal

XX pathogenic species in a sample. The method involves hybridizing a nucleic

XX acid of a fungal pathogen possibly present in the sample with at least

XX one oligonucleotide probe, from an internal Transcribed Spacer (ITS)

XX region. The method is useful for simultaneous detection and

XX differentiation of clinically important fungi in a single assay,

XX particularly *Candida albicans*, *C. parapsilosis*, *C. tropicalis*, *C. kefyr*,

XX *C. krusei*, *C. glabrata*, *C. dubliniensis*, *Aspergillus flavus*, *A.*

XX *versicole*, *A. nidulans*, *A. fumigatus*, *C. neoformans* and *pneumocystis*

XX *carinii*. The method is especially useful in the detection of

XX opportunistic infections in patients with impaired immunity systems, such

XX as organ transplant patients, patients receiving intensive anticancer

XX treatments, diabetics or AIDS patients

XX Sequence 18 BP; 3 A; 6 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
 |||||
 DB 6 TCGTCTCTCCAG 17

RESULT 193

ABK72521
 ID ABK72521 standard; DNA; 18 BP.

XX ABK72521;

DT 13-AUG-2002 (first entry)

DE DNA sequence #19 relating to nucleic acid base sequence analysis method.

XX Nucleic acid base sequence analysis; DNA diagnosis; ds.

XX Synthetic.

XX WO200233068-A1.

PD 25-APR-2002.
 XX
 PF 18-OCT-2000; 2000WO-JP007244.
 XX
 PR 18-OCT-2000; 2000WO-JP007244.
 XX
 PA (CANO) CANON KK.
 XX
 PI Yamamoto N, Okamoto T, Suzuki T;
 XX
 DR WPI; 2002-372310/40.
 XX
 PT Screening an unknown base sequence at a defined site of a target single-
 PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
 PT DNA chip, fluorescence yield and pattern-based method.
 XX
 PS Disclosure; Page 8; 53pp; Japanese.
 XX
 CC The present invention relates to a method of analysing an unknown nucleic
 CC acid base sequence. The method comprises preparing a probe array,
 CC hybridising with the probe array, measuring the fluorescence yield in the
 CC reaction, obtaining a template pattern, producing a sample pattern, and
 CC comparing the sample pattern with the template pattern. The method is
 CC useful for specifying an unknown base sequence at a defined site of a
 CC target single-stranded nucleic acid, which is useful for analysing a
 CC nucleic acid base sequence. The method is applicable in DNA diagnosis and
 CC therapy, and is useful in medicine and biology. Measuring the
 CC fluorescence yield allows the detection of a one-base mismatch which can
 CC be considered to produce high detection accuracy. The hybrid pattern of
 CC the DNA probe is used so the difference in thermostability is less
 CC important, and the judgement on each spot can be reliably carried out.
 CC ABK72503-ABK72524 represent DNA sequences described in the specification
 CC of the present invention
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ATGAACCGGAGG 27
 DB 1 ATGAACCGGAGG 12
 XX
 RESULT 194
 ABK72480/C
 ID ABK72480 standard; DNA; 18 BP.
 XX
 AC ABK72480;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Sample origonucleotide #42 for analysing nucleic acid base sequence.
 XX
 KM Nucleic acid base sequence analysis; DNA diagnosis; probe; ss.
 XX
 OS Synthetic.
 XX
 PN WO200233068-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 18-OCT-2000; 2000WO-JP007244.
 XX
 PR 18-OCT-2000; 2000WO-JP007244.
 XX
 PA (CANO) CANON KK.
 XX
 PI Yamamoto N, Okamoto T, Suzuki T;
 XX
 DR WPI; 2002-372310/40.
 XX

PT Screening an unknown base sequence at a defined site of a target single-
 PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
 PT DNA chip, fluorescence yield and pattern-based method.
 XX
 PS Example 1; Page 13; 53pp; Japanese.
 XX
 CC The present invention relates to a method of analysing an unknown nucleic
 CC acid base sequence. The method comprises preparing a probe array,
 CC hybridising with the probe array, measuring the fluorescence yield in the
 CC reaction, obtaining a template pattern, producing a sample pattern, and
 CC comparing the sample pattern with the template pattern. The method is
 CC useful for specifying an unknown base sequence at a defined site of a
 CC target single-stranded nucleic acid, which is useful for analysing a
 CC nucleic acid base sequence. The method is applicable in DNA diagnosis and
 CC therapy, and is useful in medicine and biology. Measuring the
 CC fluorescence yield allows the detection of a one-base mismatch which can
 CC be considered to produce high detection accuracy. The hybrid pattern of
 CC the DNA probe is used so the difference in thermostability is less
 CC important, and the judgement on each spot can be reliably carried out.
 CC ABK72439-ABK72502 represent sample origonucleotides used in the present
 CC invention
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ATGAACCGGAGG 27
 DB 18 ATGAACCGGAGG 7
 XX
 RESULT 195
 ABK72522/C
 ID ABK72522 standard; DNA; 18 BP.
 XX
 AC ABK72522;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE DNA sequence #20 relating to nucleic acid base sequence analysis method.
 XX
 KM Nucleic acid base sequence analysis; DNA diagnosis; ds.
 XX
 OS Synthetic.
 XX
 PN WO200233068-A1.
 XX
 PD 25-APR-2002.
 XX
 PF 18-OCT-2000; 2000WO-JP007244.
 XX
 PR 18-OCT-2000; 2000WO-JP007244.
 XX
 PA (CANO) CANON KK.
 XX
 PI Yamamoto N, Okamoto T, Suzuki T;
 XX
 DR WPI; 2002-372310/40.
 XX
 PT Screening an unknown base sequence at a defined site of a target single-
 PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
 PT DNA chip, fluorescence yield and pattern-based method.
 XX
 PS Disclosure; Page 8; 53pp; Japanese.
 XX
 CC The present invention relates to a method of analysing an unknown nucleic
 CC acid base sequence. The method comprises preparing a probe array,
 CC hybridising with the probe array, measuring the fluorescence yield in the
 CC reaction, obtaining a template pattern, producing a sample pattern, and
 CC comparing the sample pattern with the template pattern. The method is
 CC useful for specifying an unknown base sequence at a defined site of a

CC target single-stranded nucleic acid, which is useful for analysing a
 CC nucleic acid base sequence. The method is applicable in DNA diagnosis and
 CC therapy, and is useful in medicine and biology. Measuring the
 CC fluorescence yield allows the detection of a one-base mismatch which can
 CC be considered to produce high detection accuracy. The hybrid pattern of
 CC the DNA probe is used so the difference in thermostability is less
 CC important, and the judgement on each spot can be reliably carried out.
 CC ABK72503-ABK72524 represent DNA sequences described in the specification
 CC of the present invention

XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 7

Db

RESULT 196
 ABL54942/c
 ID ABL54942 standard; DNA; 18 BP.

XX
 ABL54942/c

XX
 ABL54942/c

XX
 ABL54942/c

XX
 ABL54942/c

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 ABL54942/c

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 ABL54942/c

XX
 ABL54942/c

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 ABL54942/c

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 ABL54942/c

XX
 ABL54942/c

XX
 ABL54942/c

ID ABL54942 standard; DNA; 18 BP.

XX ABL54942;

XX 18-JUN-2002 (first entry)

XX Human tumour suppressor gene p53 probe #42.

XX Human; p53; probe; variation detection; DNA array; ss.

XX Homo sapiens.

XX EPI184467-A2.

XX 06-MAR-2002.

XX 31-AUG-2001; 2001EP-00307415.

XX 31-AUG-2000; 2000JP-00263396.

XX (CANO) CANON KK.

XX Yamamoto N, Okamoto T, Tanaka S, Suzuki T;

XX WPI; 2002-271043/32.

XX Screening for gene variation by using DNA array in which probes giving
 XX strong signals forming hybrids with normal sequence, and probes having
 XX sequences expected to form hybrids with variants are separately arranged.

XX Example 2; Page 6; 22pp; English.

XX The sequence represents a full match probe designed to detect a variation
 XX a specific base in the p53 gene sequence. The invention relates to a
 XX novel method for screening for a variation in a nucleic acid sequence.

XX The method involves using a DNA array in which a group of probes which
 XX will give strong signals forming hybrids with a normal gene sequence, and
 XX a group of probes having sequences expected to form hybrids with gene
 XX variants are separately arranged. The method is useful for screening for
 XX the presence or absence of variation in a nucleic acid sequence. The
 XX method is also useful for mass screening to determine rapidly the
 XX presence or absence of a gene variation without need of an expensive
 XX apparatus and a complex analysis

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match 2.0%; Score 12; DB 6; Length 18;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;

XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGGAGG 27
 |||||
 18 ATGAACCGGAGG 7

Db

RESULT 198
 ABL54965

XX ABL54965 standard; DNA; 18 BP.

XX ABL54965;

XX 18-JUN-2002 (first entry)

XX Human rhodamine labelled p53 gene fragment #65 (normal sequence).

XX Human; p53; rhodamine; variation detection; DNA array; ss.

XX Homo sapiens.

XX Key modified_base 1

XX Location/Qualifiers

XX /*tag= a

XX /note= "Rhodamine labelled"

XX

XX

XX

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XX  EPI184467-A2.
XX
XX  06-MAR-2002.
XX
XX  31-AUG-2001; 2001EP-00307415.
XX
XX  31-AUG-2000; 2000JP-00263396.
XX
XX  (CANO ) CANON KK.
XX
XX  Yamamoto N, Okamoto T, Tanaka S, Suzuki T;
XX  WPI; 2002-271043/32.
XX
XX  Screening for gene variation by using DNA array in which probes giving
XX  strong signals forming hybrids with normal sequence, and probes having
XX  sequences expected to form hybrids with variants are separately arranged.
XX
XX  Example 2; Page 9; 22pp; English.
XX
XX  The sequence represents a section of the normal p53 gene, designated DNA
XX  #65. The sequence was used as a target for hybridisation in the
XX  invention, and hybridises to probe #42. The invention relates to a novel
XX  method for screening for a variation in a nucleic acid sequence. The
XX  method involves using a DNA array in which a group of probes which will
XX  give strong signals forming hybrids with a normal gene sequence, and a
XX  group of probes having sequences expected to form hybrids with gene
XX  variants are separately arranged. The method is useful for screening for
XX  the presence or absence of variation in a nucleic acid sequence. The
XX  method is also useful for mass screening to determine rapidly the
XX  presence or absence of a gene variation without need of an expensive
XX  apparatus and a complex analysis
XX
XX  Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX  Query Match      2.0%; Score 12; DB 6; Length 18;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  16 ATGAACCGGAGG 27
XX  |||||
XX  1 ATGAACCGGAGG 12
XX
XX  RESULT 199
XX  ID ABL58276 standard; DNA; 18 BP.
XX
XX  ABL58276;
XX
XX  15-JUL-2002 (first entry)
XX
XX  Base oligonucleotide for preparation of a probe.
XX
XX  Liquid discharge; nucleic acid analysis; gene examination; probe; ss.
XX
XX  Synthetic.
XX
XX  EPI188475-A2.
XX
XX  20-MAR-2002.
XX
XX  18-SEP-2001; 2001EP-00307932.
XX
XX  19-SEP-2000; 2000JP-00284046.
XX
XX  19-FEB-2001; 2001JP-00042344.
XX
XX  (CANO ) CANON KK.
XX
XX  Okamoto T, Yamamoto N, Watanabe H, Suzuki T;
XX  WPI; 2002-364388/40.

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XX  Producing probe supports for use in base sequence analysis of gene
XX  deoxyribonucleic acid, involves providing liquid discharging device for
XX  two-dimensionally arranging and fixing probe arrays on solid-phase
XX  substrates.
XX
XX  Disclosure; Page 20; 53pp; English.
XX
XX  The invention relates to producing a probe support. The method involves
XX  (a) providing a liquid discharging device including reservoirs for
XX  containing liquids containing the probes and discharge nozzles for
XX  with the corresponding reservoirs; (b) aligning the discharge nozzles and
XX  the support relatively; and (c) discharging the liquids containing the
XX  probes from the discharge nozzles to different positions on the support.
XX  The number of reservoirs and discharge nozzles are the number of probes.
XX  The method is useful for producing probe supports useful in base sequence
XX  analysis of gene deoxyribonucleic acid (DNAs) and gene examination. The
XX  present sequence represents a base oligonucleotide used for preparation
XX  of a probe
XX
XX  Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX  Query Match      2.0%; Score 12; DB 6; Length 18;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX  Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  16 ATGAACCGGAGG 27
XX  |||||
XX  1 ATGAACCGGAGG 12
XX
XX  RESULT 200
XX  ID ABR88543 standard; DNA; 18 BP.
XX
XX  ABR88543;
XX
XX  07-OCT-2002 (first entry)
XX
XX  Synthetic hybridisation probe for nucleic acid detection method.
XX
XX  Probe nucleic acid; target nucleic acid; hybrid; nucleic acid detection;
XX  ss.
XX
XX  Synthetic.
XX
XX  JP2002176999-A.
XX
XX  25-JUN-2002.
XX
XX  12-DEC-2000; 2000JP-00377349.
XX
XX  12-DEC-2000; 2000JP-00377349.
XX
XX  (CANO ) CANON KK.
XX
XX  WPI; 2002-569947/61.
XX
XX  Detecting nucleic acid with hybrid formation of a probe nucleic acid and
XX  a target nucleic acid without interference of the other double stranded
XX  nucleic molecules.
XX
XX  Example 1; Page 9; 13pp; Japanese.
XX
XX  The invention describes a hybrid of a probe nucleic acid and a target
XX  nucleic acid for detection of nucleic acid. This sequence represents a
XX  synthetic hybridisation probe used in the nucleic acid detection method of
XX  the invention
XX
XX  Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX  Query Match      2.0%; Score 12; DB 6; Length 18;
XX  Best Local Similarity 100.0%; Pred. No. 1.2e+05;

```

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
 XX |||||
 DB 1 ATGACCGGAGG 12

RESULT 201
 ABR8542/c
 ID ABR8542 standard; DNA; 18 BP.
 XX
 AC ABR8542;
 XX
 DT 07-OCT-2002 (first entry)
 XX

DE Synthetic target gene fragment for nucleic acid detection method #1.

KM Probe nucleic acid; target nucleic acid; hybrid; nucleic acid detection;
 XX ss.

XX Synthetic.

XX PN JP2002176999-A.

XX PD 25-JUN-2002.

XX PF 12-DEC-2000; 2000JP-00377349.

XX PR 12-DEC-2000; 2000JP-00377349.

XX PA (CANO) CANON KK.

XX DR WPI; 2002-569947/61.

PT Detecting nucleic acid with hybrid formation of a probe nucleic acid and
 PT a target nucleic acid without interference of the other double stranded
 PT nucleic molecules.

XX PS Example 1; Page 9; 13pp; Japanese.

CC The invention describes a hybrid of a probe nucleic acid and a target
 CC nucleic acid for detection of nucleic acid. This sequence represents a
 CC synthetic target gene fragment for probe hybridisation used in the nucleic
 CC acid detection method of the invention

XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred.No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
 XX |||||
 DB 18 ATGACCGGAGG 7

RESULT 202
 ABR04735/c
 ID ABR04735 standard; DNA; 18 BP.
 XX
 AC ABR04735;
 XX

DT 27-SEP-2002 (first entry)
 XX

DE End-labelled probe array production method-related oligonucleotide 42.

XX End-labelled probe array production; probe; ss; target substance capture.

XX Unidentified.

XX JP2002153284-A.

XX PD 28-MAY-2002.

XX PF 24-NOV-2000; 2000JP-00357446.
 XX PR 24-NOV-2000; 2000JP-00357446.
 XX PA (CANO) CANON KK.

XX DR WPI; 2002-552742/59.

PT Preparation of an end-labelled probe array, for capturing a target
 PT substance.

XX PS Example 1; Page 5; 25pp; Japanese.

CC The invention comprises a method for the synthesis of an end-labelled
 CC probe array - in which part of a probe for capturing a target substance
 CC is fixed at a plural of the matrix sites on the surface of a probe array
 CC substrate. In the method of the invention the units for constituting the
 CC probe are combined successively and, at the final stage of the successive
 CC synthesis, a labelling substance is combined to the end of the probe and
 CC extended to a desired chain length. The method of the invention is useful
 CC for the production of a probe array. The present DNA sequence represents
 CC an oligonucleotide that was used in an example of the invention

XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred.No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGACCGGAGG 27
 XX |||||
 DB 18 ATGACCGGAGG 7

RESULT 203
 ABR04758
 ID ABR04758 standard; DNA; 18 BP.
 XX
 AC ABR04758;
 XX

DT 27-SEP-2002 (first entry)
 XX

DE End-labelled probe array production method-related oligonucleotide 65.

XX End-labelled probe array production; probe; ss; target substance capture.

XX OS Unidentified.

XX PN JP2002153284-A.

XX PD 28-MAY-2002.

XX PF 24-NOV-2000; 2000JP-00357446.

XX PR 24-NOV-2000; 2000JP-00357446.

XX PA (CANO) CANON KK.

XX DR WPI; 2002-552742/59.

PT Preparation of an end-labelled probe array, for capturing a target
 PT substance.

XX PS Example 1; Fig 1; 25pp; Japanese.

CC The invention comprises a method for the synthesis of an end-labelled
 CC probe array - in which part of a probe for capturing a target substance
 CC is fixed at a plural of the matrix sites on the surface of a probe array
 CC substrate. In the method of the invention the units for constituting the
 CC probe are combined successively and, at the final stage of the successive
 CC synthesis, a labelling substance is combined to the end of the probe and
 CC extended to a desired chain length. The method of the invention is useful

CC for the production of a probe array. The present DNA sequence represents
CC an oligonucleotide that was used in an example of the invention

XX Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGAGG 27

Db 1 ATGAACCGAGG 12

RESULT 204

ABQ81304/c

ID ABQ81304 standard; DNA; 18 BP.

XX ABQ81304;

XX 12-DEC-2002 (first entry)

DE Cytochrome P450 CYP2A6 sense primer.

KM Cytochrome P450; CYP2A6; enzyme; tachyphylaxis; drug tolerance; human;

XX psoriasis; antipsoriatic; antipruritic; dermatological; PCR; primer; ss.

OS Homo sapiens.

XX WO200245704-A2.

XX 13-JUN-2002.

PF 04-DEC-2001; 2001WO-GB005369.

XX 04-DEC-2000; 2000GB-00029524.

PA (MOLE-) MOLECULAR SKINCARE LTD.

PI Adcocks C, Bavić C, Cork M, Duff G, Tazi-Ahimi R, Ward S;

DR WPI; 2002-713334/77.

PT Alluviating or preventing a tachyphylactic response to an agent and
PT treating psoriasis, comprises administering an antagonist of a metabolic
PT enzyme, which is induced as a result of exposure to the agent, to a
PT patient.

PS Example 1; Page 75; 136pp; English.

XX The present sequence is a sense primer for cytochrome P450 CYP2A6. RT-PCR
CC was used to characterise metabolic enzyme induction by vitamin D
CC analogues, corticosteroids and macrobiacams in human skin. The invention
CC provides for the use of antagonists of P450 enzymes for the prevention or
CC alleviation of a tachyphylactic response to administration of a vitamin D
CC analogue, corticosteroid or macrobiacam to a patient, e.g. for the
CC treatment of psoriasis. The underlying cause of tachyphylaxis was shown
CC to be degradation of a drug in the patient, rather than desensitization
CC or receptor down-regulation. Exposure of a patient to the drug for
CC extended periods results in an increase in the expression of enzymes
CC which are capable of metabolizing the drug. A method for treatment of
CC tachyphylaxis therefore involves inhibiting the induced metabolic enzyme,
CC especially a P450 cytochrome, by administration of an antagonist of the
CC enzyme. Detection of an increase in the amount and/or activity of a
CC metabolic enzyme capable of metabolizing a drug following extended
CC exposure of a cell from an individual to the drug indicates the increased
CC likelihood of that individual developing a tachyphylactic response to the
CC drug

XX Sequence 18 BP; 8 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 TTGCTCTTCTC 186

Db 16 TTGCTCTTCTC 5

RESULT 205

ABL59677/c

ID ABL59677 standard; DNA; 18 BP.

XX ABL59677;

XX 18-JUL-2002 (first entry)

DE Oligonucleotide probe SEQ ID NO:42.

XX Simultaneous determination; probe; ss.

XX Synthetic.

XX JP2002065299-A.

XX 05-MAR-2002.

XX 31-AUG-2000; 2000JP-00263505.

XX 31-AUG-2000; 2000JP-00263505.

XX (CANO) CANON KK.

XX WPI; 2002-398978/43.

PT Simultaneous testing of the reactivity of a sample with other different
PT samples, comprises applying to the two samples to a substrate comprising
PT divided matrices.

PS Example 1; Page 11; 24pp; Japanese.

XX The present invention describes a method for determining simultaneously
CC the reactivity of a first sample with other samples, in which the second
CC to the 2 plus n-th (n is not less than 1) samples having different
CC properties are arranged independently on a substrate, on whose surface
CC the first sample is already present, and the reactivities between the
CC first sample and each of the second to the 2 plus n-th samples are
CC determined. Also described is a tissue sample matrix in which several
CC samples from different sources are present on each matrix divided on a
CC substrate. The method is used for determining simultaneously the
CC reactivity of a first sample with several other differing samples.

CC ABL59636 to ABL59701 represent oligonucleotide probes used in an example
CC from the present invention

XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGAACCGAGG 27

Db 18 ATGAACCGAGG 7

RESULT 206

ABT06256/c

ID ABT06256 standard; DNA; 18 BP.

XX ABT06256;

XX 24-OCT-2002 (first entry)

DE Synthetic DNA selling system - related oligonucleotide 61.

KW Synthetic DNA selling system; internet; ss; purchase order menu;
 XX major histocompatibility complex; MHC.
 OS Synthetic.
 XX JP2002074089-A.
 XX
 XX 12-MAR-2002.
 XX
 XX 29-AUG-2000; 2000JP-00259715.
 XX
 XX 29-AUG-2000; 2000JP-00259715.
 XX
 XX (CANO) CANON KK.
 XX
 XX WPI; 2002-492955/53.
 XX
 XX Synthetic DNA selling system using the internet; displays purchase order
 PT menu to orderer's terminal and initiates production of selected DNA for
 PT the successful bidder.
 XX
 XX Disclosure; Fig 5; 22pp; Japanese.
 XX
 XX The invention comprises a synthetic DNA selling system using the
 CC internet. The system displays a purchase order menu display, with the
 CC number of base sequences of DNA from which the orderer selects a DNA. The
 CC order information is transmitted to a successful bidder side server which
 CC orders for production and delivery of selected synthetic DNA. The system
 CC of the invention is useful for marketing synthetic DNAs of different base
 CC sequences and concentrations according to the desire of the user,
 CC especially genes concerned with human major histocompatibility complex
 CC (MHC). Oligonucleotides ABT06196 - ABT06278 are used in the invention
 XX
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ATGACCGGAGG 27
 DB 18 ATGACCGGAGG 7
 RESULT 207
 AAD51874
 ID AAD51874 standard; DNA; 18 BP.
 XX
 AC AAD51874;
 XX
 DT 02-MAY-2003 (first entry)
 XX
 DE Porcine interferon (IFN)-alpha DNA amplifying forward PCR primer.
 XX
 KM Porcine; interferon; IFN; foot and mouth disease; vaccine; immunisation;
 KM FMD; virulence; PCR; primer; ss.
 XX
 OS Sus sp.
 XX
 XX WO200287336-A1.
 XX
 PD 07-NOV-2002.
 XX
 XX 26-APR-2002; 2002WO-US012247.
 XX
 XX 26-APR-2001; 2001US-0286345P.
 XX
 XX 24-APR-2002; 2002US-00128463.
 XX
 XX (USDA) US SEC OF AGRIC.
 XX
 XX Grubman MJ, Chinsangara J, Koester M, Moraes MP;
 XX WPI; 2003-140146/13.
 DR

XX
 XX New construct comprising a DNA sequence capable of expressing interferon
 PT in animals susceptible to foot and mouth disease, useful for preparing a
 PT vaccine for providing protective immunization against foot and mouth
 PT disease.
 XX
 XX Example 3; Page 71; 72pp; English.
 XX
 XX The invention relates to a novel construct comprising a DNA sequence
 CC capable of expressing interferon (IFN) in animals susceptible to foot and
 CC mouth disease (FMD). The construct, vaccine and method are useful for
 CC protective immunisation against foot and mouth disease in animals. The
 CC construct is useful for preparing a vaccine, which is particularly useful
 CC for stimulating protective response to such disease. The present sequence
 CC is porcine interferon (pIFN)-alpha DNA amplifying PCR primer. This
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 18 BP; 4 A; 9 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 303 CCCCAACTCAG 314
 DB 5 CCCCAACTCAG 16
 RESULT 208
 AB221481
 ID AB221481 standard; DNA; 18 BP.
 XX
 AC AB221481;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE Synthetic probe SEQ ID NO 1.
 XX
 KM Probe array; probe; ss.
 XX
 OS Synthetic.
 XX
 XX JP2002253251-A.
 XX
 PD 10-SEP-2002.
 XX
 XX 28-FEB-2001; 2001JP-00055972.
 XX
 XX 28-FEB-2001; 2001JP-00055972.
 XX
 XX (CANO) CANON KK.
 XX
 XX WPI; 2003-096532/09.
 XX
 DR A process for preparation of a high density array of probes, used for DNA
 PT analysis and screening, comprising solution dropped on a carrier to form
 PT multiple spots at high speed.
 XX
 XX Example 3; Page 12; 19pp; Japanese.
 XX
 XX The invention relates to preparation of a probe array by high speed and
 CC accurate dropping of the probe solution to improve quality of the probe
 CC array. The probe array is useful in the analysis of base sequences of DNA
 CC and reliable genetic screening of multiple items. The present sequence is
 CC that of a probe used in examples of the invention
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 2.0%; Score 12; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 ATGACCGGAGG 27

Db 1 ATGAACCGAGG 12

RESULT 209
AB221482/C
ID AB221482 standard; DNA; 18 BP.
XX
AC AB221482;
XX
DT 28-MAR-2003 (first entry)
XX
DE Synthetic probe SEQ ID NO 2.
XX
KM Probe array; probe; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "G-OP03-(CH2)6-SH"
XX
XX JP2002253251-A.
XX
XX 10-SEP-2002.
XX
XX 28-FEB-2001; 2001JP-00055972.
XX
XX 28-FEB-2001; 2001JP-00055972.
XX
XX (CANO) CANON KK.
XX
XX WPI; 2003-096532/09.
XX
XX A process for preparation of a high density array of probes, used for DNA
XX analysis and screening, comprising solution dropped on a carrier to form
XX multiple spots at high speed.
XX
XX Example 3; Page 12; 19pp; Japanese.
XX
XX The invention relates to preparation of a probe array by high speed and
XX accurate dropping of the probe solution to improve quality of the probe
XX array. The probe array is useful in the analysis of base sequences of DNA
XX and reliable genetic screening of multiple items. The present sequence is
XX that of a probe used in examples of the invention
XX
XX Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
DB 18 ATGAACCGAGG 7

RESULT 210
ABV77868
ID ABV77868 standard; DNA; 18 BP.
XX
AC ABV77868;
XX
DT 24-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID 1 used to prepare a probe.
XX
KM Probe; probe carrier; DNA micro-chip; ss.
XX
OS Synthetic.
XX

FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5' labelled with tetramethyl rhodamine"

XX JP2002257694-A.
XX
XX 11-SEP-2002.
XX
XX 28-FEB-2001; 2001JP-00055970.
XX
XX 28-FEB-2001; 2001JP-00055970.
XX
XX (CANO) CANON KK.
XX
XX WPI; 2003-079066/08.
XX
XX Device for manufacturing a probe carrier used for analyzing base sequence
XX of genetic DNA comprises discharging liquid through a group of
XX discharging openings on each probe spot.
XX
XX Example 4; Page 12; 18pp; Japanese.
XX

XX The present invention relates to a device for manufacturing a probe
XX carrier with some types of probes. The device comprises: (i) a solution
XX discharge unit composed of reservoirs for housing the respective types of
XX probe solutions; (ii) groups of discharging openings connected to the
XX respective reservoirs; and (iii) discharging energy generating members
XX corresponding to the respective discharging openings one by one. The
XX device is suitable for manufacturing probe carriers, such as, DNA micro-
XX chips etc. used for analysing base sequence of genetic DNA etc. The
XX present sequence is a oligonucleotide used for preparing a probe, which
XX was used in an example from the invention

SO Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGAACCGAGG 27
DB 1 ATGAACCGAGG 12

RESULT 211
ABV77869/C
ID ABV77869 standard; DNA; 18 BP.
XX
AC ABV77869;
XX
DT 24-FEB-2003 (first entry)
XX
DE Oligonucleotide SEQ ID 2 used to prepare a probe.
XX
KM Probe; probe carrier; DNA micro-chip; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5' labelled with SH-(CH2)6-PO4"

XX JP2002257694-A.
XX
XX 11-SEP-2002.
XX
XX 28-FEB-2001; 2001JP-00055970.
XX
XX 28-FEB-2001; 2001JP-00055970.
XX
XX

XX (CANO) CANON KK.
 PA WPI; 2003-079066/08.
 XX
 DR
 XX
 PT Device for manufacturing a probe carrier used for analyzing base sequence
 PT of genetic DNA comprises discharging liquid through a group of
 PT discharging openings on each probe spot.
 XX
 PS Example 4; Page 12; 18pp; Japanese.
 XX
 CC The present invention relates to a device for manufacturing a probe
 CC carrier with some types of probes. The device comprises: (i) a solution
 CC discharge unit composed of reservoirs for housing the respective types of
 CC probe solutions; (ii) groups of discharging openings connected to the
 CC respective reservoirs; and (iii) discharging energy generating members
 CC corresponding to the respective discharging openings one by one. The
 CC device is suitable for manufacturing probe carriers, such as, DNA micro-
 CC chips etc. used for analyzing base sequence of genetic DNA etc. The
 CC present sequence is a oligonucleotide used for preparing a probe, which
 CC was used in an example from the invention. Note: This sequence is shown
 CC in this orientation (5' to 3') in the disclosure of the specification.
 CC but is shown in the opposite orientation in the sequence listing
 SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 QY
 Query Match 2.0%; Score 12; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16 ATGACCGGAGG 27
 18 ATGACCGGAGG 7
 RESULT 212
 AAL51414
 ID AAL51414 standard; DNA; 18 BP.
 XX
 AC AAL51414;
 XX
 DT 27-MAR-2003 (first entry)
 DE Probe carrier manufacturing method-related oligonucleotide, SEQ ID NO 1.
 XX
 KM Probe; ss; probe carrier manufacture; DNA micro-chips.
 XX
 OS Unidentified.
 XX
 PN JP200257836-A.
 XX
 PD 11-SEP-2002.
 XX
 PF 28-FEB-2001; 2001JP-00055971.
 XX
 PR 28-FEB-2001; 2001JP-00055971.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2003-106341/10.
 XX
 PT Manufacturing a probe carrier used for analyzing a base sequence of
 PT genetic DNA, comprises discharging a probe solution in a cavity located
 PT at each probe position on a probe carrier through a group of discharging
 PT openings.
 XX
 PS Example 4; Page 12; 18pp; Japanese.
 XX
 CC The invention comprises a method for manufacturing a probe carrier. The
 CC method involves discharging and fixing probe solutions in the
 CC corresponding cavities according to information on the positions of
 CC respective types of probes. The method of the invention is useful for
 CC manufacturing probe carriers (e.g. DNA micro-chips). The present DNA

CC sequence represents an oligonucleotide used in the method of the
 CC invention
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 QY
 Query Match 2.0%; Score 12; DB 7; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16 ATGACCGGAGG 27
 1 ATGACCGGAGG 12
 RESULT 213
 ADC54006
 ID ADC54006 standard; DNA; 18 BP.
 XX
 AC ADC54006;
 XX
 DT 18-DEC-2003 (first entry)
 DE Oligonucleotide of the invention SEQ ID NO:1.
 XX
 KM ss; probe carrier; discharge.
 XX
 OS Synthetic.
 XX
 PN JP2003035711-A.
 XX
 PD 07-FEB-2003.
 XX
 PF 28-MAR-2002; 2002JP-00093023.
 XX
 PR 28-MAR-2001; 2001JP-00094400.
 XX
 PA (CANO) CANON KK.
 XX
 DR WPI; 2003-535999/51.
 XX
 PT Probe carrier manufacturing method for inkjet system, involves scanning
 PT liquid discharge head in direction orthogonal to scanning direction, at
 PT angle satisfying predetermined relation.
 XX
 PS Example 2; SEQ ID NO 1; 17pp; Japanese.
 XX
 CC The invention relates to a novel probe carrier and the method for
 CC manufacturing the carrier. The invention enables stable discharge of
 CC solution, and removes liquid droplets adhering to discharge nozzle. The
 CC present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 18 BP; 5 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 QY
 Query Match 2.0%; Score 12; DB 9; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 16 ATGACCGGAGG 27
 1 ATGACCGGAGG 12
 RESULT 214
 ADC54007/C
 ID ADC54007 standard; DNA; 18 BP.
 XX
 AC ADC54007;
 XX
 DT 18-DEC-2003 (first entry)
 DE Oligonucleotide of the invention SEQ ID NO:2.
 XX
 KM ss; probe carrier; discharge.


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XX OS Synthetic.
XX XX JP2003035711-A.
XX PD 07-FEB-2003.
XX PF 28-MAR-2002; 2002JP-00093023.
XX PR 28-MAR-2001; 2001JP-00094400.
XX PA (CANO ) CANON KK.
XX DR WPI; 2003-535999/51.
XX PT Probe carrier manufacturing method for inkjet system, involves scanning
XX PT liquid discharge head in direction orthogonal to scanning direction, at
XX PT angle satisfying predetermined relation.
XX PS Example 2; SEQ ID NO 2; 17pp; Japanese.
XX CC The invention relates to a novel probe carrier and the method for
XX CC manufacturing the carrier. The invention enables stable discharge of
XX CC solution, and removes liquid droplets adhering to discharge nozzle. The
XX CC present sequence is used in the exemplification of the invention.
XX SQ Sequence 18 BP; 2 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 9; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 ATGAACCGAGG 27
   |||||
Db 18 ATGAACCGAGG 7

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RESULT 215
AAT43666
ID AAT43666 standard; DNA; 19 BP.
XX AC AAT43666;
XX DT 19-AUG-1997 (first entry)
XX DE HIV-1 matrix protein p17 gene probe 3.
XX KM Human immunodeficiency virus type 1; subtype B; transmissible;
XX KM matrix protein p17; prognosis; probe; detection; maternal transmission;
XX KM hybridisation assay; immunoassay; ss.
XX OS Synthetic.
XX PN EP743364-A2.
XX PD 20-NOV-1996.
XX PF 17-MAY-1996; 96EP-00401084.
XX PR 18-MAY-1995; 95FR-00005914.
XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX PI Narwa R, Roques P;
XX DR WPI; 1996-507733/51.
XX PT Human immunodeficiency virus p17 gene fragments, derived proteins and
XX PT antibodies - useful for assessing the risk of maternal transmission of
XX PT HIV-1 infection.
XX PS Claim 15; Page 29; 46pp; French.

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CC CC A set of six oligonucleotide probes enable the risk of maternal- foetal
CC CC transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
CC CC AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
CC CC transmitted to the foetus; probes 2-4 (see AAT43665-T43668) allow
CC CC detection of strains which are never transmitted from mother to foetus.
CC CC The present sequence is that of probe 3 and it detects PAL, HMI, AWO,
CC CC CHER, GOR, MOE, SIM, FLO, 2759, 2826, 4501, 4538 and 5613 HIV-1 sequences
XX SQ Sequence 19 BP; 1 A; 6 C; 3 G; 9 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
   |||||
Db 4 TTGCTCTTCCTC 15

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RESULT 216
AAT43665
ID AAT43665 standard; DNA; 19 BP.
XX AC AAT43665;
XX DT 19-AUG-1997 (first entry)
XX DE HIV-1 matrix protein p17 gene probe 2.
XX KM Human immunodeficiency virus type 1; subtype B; transmissible;
XX KM matrix protein p17; prognosis; probe; detection; maternal transmission;
XX KM hybridisation assay; immunoassay; ss.
XX OS Synthetic.
XX PN EP743364-A2.
XX PD 20-NOV-1996.
XX PF 17-MAY-1996; 96EP-00401084.
XX PR 18-MAY-1995; 95FR-00005914.
XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX PI Narwa R, Roques P;
XX DR WPI; 1996-507733/51.
XX PT Human immunodeficiency virus p17 gene fragments, derived proteins and
XX PT antibodies - useful for assessing the risk of maternal transmission of
XX PT HIV-1 infection.
XX PS Claim 15; Page 29; 46pp; French.
XX CC A set of six oligonucleotide probes enable the risk of maternal- foetal
XX CC transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
XX CC AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
XX CC transmitted to the foetus; probes 2-4 (see AAT43665-T43668) allow
XX CC detection of strains which are never transmitted from mother to foetus.
XX CC The present sequence is that of probe 2 and it detects HAR, LOUB, VIL and
XX CC 2754 HIV-1 sequences
XX SQ Sequence 19 BP; 1 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match          2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 175 TTGCTCTTCCTC 186
   |||||
Db 4 TTGCTCTTCCTC 15

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RESULT 217
PD AAT43667
XX ID AAT43667 standard; DNA; 19 BP.
XX PF AAT43667;
XX PR 19-AUG-1997 (first entry)
XX PA 19-AUG-1997 (first entry)
XX PI HIV-1 matrix protein p17 gene probe 4.
XX DE HIV-1 matrix protein p17 gene probe 4.
XX KM Human immunodeficiency virus type 1; subtype B; transmissible;
XX matrix protein p17; prognosis; probe; detection; maternal transmission;
XX hybridisation assay; immunosay; ss.
XX OS Synthetic.
XX PN EP743364-A2.
XX PD 20-NOV-1996.
XX PF 17-MAY-1996; 96EP-00401084.
XX PR 18-MAY-1995; 95PR-00005914.
XX PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.
XX PI Narwa R, Roques P;
XX DR WPI; 1996-507733/51.
XX PT Human immunodeficiency virus p17 gene fragments, derived proteins and
XX antibodies - useful for assessing the risk of maternal transmission of
XX HIV-1 infection.
XX PS Claim 15; Page 29; 46pp; French.
XX CC A set of six oligonucleotide probes enable the risk of maternal- foetal
XX transmission of subtype B HIV-1 to be evaluated. Probes 1 and 6 (see
XX AAT43664 and AAT43669) allow detection of HIV-1 strains which are always
XX transmitted to the foetus; probes 2-4 (see AAT43665-743668) allow
XX detection of strains which are never transmitted from mother to foetus.
XX CC The present sequence is that of probe 4 and it detects the CEL HIV-1
XX sequence
XX SQ Sequence 19 BP; 1 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 TTGCTCTTCCTC 186
DB 3 TTGCTCTTCCTC 14

RESULT 218
PD AAT68898/c
XX ID AAT68898 standard; DNA; 19 BP.
XX AC AAT68898;
XX DT 06-APR-1998 (first entry)
XX DE Human beta-actin 5' RT-PCR primer.
XX KM Drug-resistance; neoplastic disease; non-malignant haematopoietic cell;
XX progenitor; gene rearrangement; RT-PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9718305-A2.

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XX PD 22-MAY-1997.
XX PF 13-NOV-1996; 96MO-US018273.
XX PR 14-NOV-1995; 95US-0006692P.
XX PA (MINTU ) UNIV MINNESOTA.
XX PI Verfallle CM, McIvor RS, Zhao RC;
XX DR WPI; 1997-289281/26.
XX PT Expression cassette for forming drug resistant hematopoietic stem cells -
XX decreases RNA or protein found only in malignant cells; for treating
XX leukaemia(s), such as chronic myelogenous leukaemia.
XX PS Example 2; Fig 1; 52pp; English.
XX CC This beta-actin 5' RT-PCR primer is used in a novel method of preparing
XX drug-resistant, non-malignant hematopoietic cells. This method involves
XX the construction of a new expression cassette comprising a first nucleic
XX acid molecule which encodes resistance of a host cell to a cytotoxic
XX agent, operably linked to a first promoter which functions in the host
XX cell and a second nucleic acid molecule operably linked to a second
XX promoter which functions in the host cell. The second nucleic acid
XX molecule encodes an RNA molecule or a polypeptide whose expression
XX decreases the expression of an RNA or a polypeptide present in a
XX malignant cell only. This method can eliminate residual neoplastic
XX disease in a patient, where the disease has an immature hematopoietic
XX progenitor cell with a well-defined gene rearrangement. Diseases such as
XX chronic myelogenous leukemia which is associated with a BCR/ABL gene
XX rearrangement, acute lymphoblastic leukemia and acute promyelocytic
XX leukemia may be treated using this method
XX SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred.No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGATCTTCA 328
DB 19 TGAGATCTTCA 8

RESULT 219
PD AAT68899/c
XX ID AAT68899 standard; DNA; 19 BP.
XX AC AAT68899;
XX DT 06-APR-1998 (first entry)
XX DE Human beta-actin 3' RT-PCR primer.
XX KM Drug-resistance; neoplastic disease; non-malignant haematopoietic cell;
XX progenitor; gene rearrangement; RT-PCR primer; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9718305-A2.
XX PD 22-MAY-1997.
XX PF 13-NOV-1996; 96MO-US018273.
XX PR 14-NOV-1995; 95US-0006692P.
XX PA (MINTU ) UNIV MINNESOTA.
XX PI Verfallle CM, McIvor RS, Zhao RC;

```

```

XX
DR WPI, 1997-289281/26.
XX
PT Expression cassette for forming drug resistant hematopoietic stem cells -
PT decreases RNA or protein found only in malignant cells; for treating
PT leukaemia(s), such as chronic myelogenous leukaemia.
XX
PS Example 2; Fig 1; 52pp; English.
XX
CC This beta-actin 3' RT-PCR primer is used in a novel method of preparing
CC drug-resistant, non-malignant hematopoietic cells. This method involves
CC the construction of a new expression cassette comprising a first nucleic
CC acid molecule which encodes resistance of a host cell to a cytotoxic
CC agent, operably linked to a first promoter which functions in the host
CC cell and a second nucleic acid molecule operably linked to a second
CC promoter which functions in the host cell. The second nucleic acid
CC molecule encodes an RNA molecule or a polypeptide whose expression
CC decreases the expression of an RNA or a polypeptide present in a
CC malignant cell only. This method can eliminate residual neoplastic
CC disease in a patient, where the disease has an immature hematopoietic
CC progenitor cell with a well-defined gene rearrangement. Diseases such as
CC chronic myelogenous leukaemia which is associated with a BCR/ABL gene
CC rearrangement acute lymphoblastic leukaemia and acute promyelocytic
CC leukaemia may be treated using this method
XX
SQ Sequence 19 BP; 6 A; 6 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 317 TGAGGATCTTCA 328
19 TGAGGATCTTCA 8
Db
RESULT 220
AAV40952/C
ID AAV40952 standard; DNA; 19 BP.
XX
AC AAV40952;
XX
DT 25-SEP-1998 (first entry)
XX
DE Primer BCRA1B:1698U9 for abnormality detection.
XX
KM PCR primer; chromosomal abnormality; abnormality detection; leukaemia;
KM lymphoma; carcinoma; adenocarcinoma; sarcoma; glioma; neuroblastoma;
KM medullablastoma; malignant melanoma; malignant neoplastic condition; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824928-A2.
XX
PD 11-JUN-1998.
XX
PF 08-DEC-1997; 97WO-DK000556.
XX
PR 06-DEC-1996; 96DK-00001401.
XX
PA (PALI/) PALISGAARD N.
PI Pallsgaard N, Hokland P;
XX
DR WPI, 1998-333344/29.
XX
PT Detection of chromosomal abnormalities - by subjecting patient sample
PT nucleic acids to a multiplex molecular amplification procedure using
PT primers specific for characteristic nucleic acid sequence.
PS Claim 73; Page 74; 126pp; English.
XX

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CC This sequence represents a primer used in the method of the invention for
CC the detection of the presence or absence of chromosomal abnormalities,
CC each abnormality being associated with a condition in a subject and each
CC being defined by at least one characteristic nucleic acid sequence. The
CC method comprises: (a) obtaining a sample of nucleic acids derived from a
CC subject which may harbour one of the chromosomal abnormalities; (b)
CC subjecting the sample to a multiplex molecular amplification (MMA)
CC procedure, where a number of the characteristic sequences, if present in
CC a sufficient amount, will be amplified; (c) retrieving the product(s)
CC from step (b), and detecting the presence and/or absence of an amplicon
CC characteristic of the abnormal sequences to detect the presence or
CC absence of corresponding chromosomal abnormalities; where the MMA
CC procedure comprises the use of at least 7 mutually distinct primers (MDP)
CC in one single reaction mixture, each of the primers defining an end of at
CC least one characteristic nucleic acid sequence, and where at least one of
CC the primers defines the first end of at least two characteristic nucleic
CC acid sequences, the characteristic nucleic acid sequences each being
CC determined in their opposite ends by MDP selected from the remainder of
CC the MDP. The methods can be used for detecting chromosomal abnormalities
CC associated with diseases including numerous leukaemia's, lymphoma's,
CC carcinoma's, adenocarcinoma's, sarcoma's, glioma's, neuroblastoma's,
CC medullablastoma, malignant melanoma, and malignant neoplastic conditions
XX
SQ Sequence 19 BP; 3 A; 9 C; 3 G; 4 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 290 TTCTGGCAGGCA 301
17 TTCTGGCAGGCA 6
Db
RESULT 221
AAA13623
ID AAA13623 standard; DNA; 19 BP.
XX
AC AAA13623;
XX
DT 20-JUL-2000 (first entry)
XX
DE Human oncofoetal ferritin 1 PCR primer #8.
XX
KM Human; oncofoetal ferritin 1; OFP1; ferritin; transplation;
KM pathological pregnancy; breast cancer; cytotoxic; immunosuppressive;
KM contraceptive; abortive; neotrophic; vaccine; immunisation; cancer;
KM transplant rejection; autoimmune disease; fertilisation; diagnosis;
KM in vitro fertilization; IVF; heptablastoma; Hodgkin's lymphoma;
KM leukaemia; non-Hodgkin's lymphoma; embryonal tumour; Down's Syndrome;
KM spontaneous abortion; miscarriage; premature contraction; toxemia;
KM premature delivery; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200015788-A2.
XX
PD 23-MAR-2000.
XX
PF 08-SEP-1999; 99WO-IL000485.
XX
PR 11-SEP-1998; 98IL-00126181.
XX
PA (GARD-) GARDINO INVESTMENT NV.
PI Moroz C;
XX
DR WPI, 2000-271427/23.
XX
PT DNA sequence coding for oncofoetal ferritin 1 protein, useful for
PT immunizations against breast cancer, for enhancing fertilization rates
PT during in vitro fertilization treatment and for use as a growth factor of
PT bone-marrow progenitor cells.
XX

```

XX Claim 23; Page 49; 66pp; English.

XX PS The present sequence represents a specifically claimed PCR primer used in

CC the isolation of oncofetal ferritin 1 (OFPI) protein. OFPI has

CC cytotactic, immunosuppressive, contraceptive, abortive and neutrotic

CC activities, and can be used as a vaccine. Compositions comprising the

CC expression vector containing an OFPI coding sequence, and the OFPI

CC protein, are useful: (a) for immunisations against cancer, especially

CC breast cancer; (b) in the treatment of transplant rejections, autoimmune

CC diseases, pathological pregnancies; (c) for enhancing fertilisation rates

CC during in vitro fertilisation (IVF) treatment; and (d) for use as a

CC growth factor of bone-marrow progenitor cells such as granulocyte

CC monocytes. The OFPI nucleotide sequence is useful for diagnosing cancer

CC such as breast cancer, hepatoblastoma, leukaemia, Hodgkin's and non-

CC Hodgkin's lymphomas and embryonal tumours, Down's Syndrome, and

CC pathological pregnancies such as spontaneous abortion and miscarriage,

CC premature contractions, toxemia or premature delivery

XX SQ Sequence 19 BP; 3 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 CTCCTCGAGCCC 257
DB 7 CTCCTCGAGCCC 18

RESULT 222
AAZ76946/c
ID AAZ76946 standard; DNA; 19 BP.

XX AC AAZ76946;

DT 10-SEP-2001 (first entry)

XX DE Human biallelic marker downstream amplification primer SEQ ID NO:11302.

XX KW Human genome; biallelic marker; high density disequilibrium map;

XX KW genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX KW haplotyping; hybridisation; identification; characterisation;

XX KW amplification; single nucleotide polymorphism; SNP; PCR primer;

XX KW diagnosis; ss.

XX OS Homo sapiens.

XX PN WO954500-A2.

XX PD 28-OCT-1999.

XX PF 21-APR-1999; 95MO-IB000822.

XX PR 21-APR-1998; 98US-0082614P.

XX PR 23-NOV-1998; 98US-0109732P.

XX PA (GEST) GENSET.

XX PI Cohen D, Blumenfeld M, Chumakov I;

XX DR WPI; 2000-013267/01.

XX PT Novel biallelic markers used to construct a high density disequilibrium

PT map of the human genome.

XX Claim 9; Page 2640; 2745pp; English.

XX AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID Nos 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

CC present invention

XX SQ Sequence 19 BP; 9 A; 1 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 TGCTCTTCCTCC 187
DB 15 TGCTCTTCCTCC 4

RESULT 223
AACT0391
ID AACT0391 standard; DNA; 19 BP.

XX AC AACT0391;

DT 09-FEB-2001 (first entry)

XX DE Single nucleotide polymorphism PCR primer #148.

XX KW Single nucleotide polymorphism; SNP; human; genetic disease;

XX KW disease susceptibility; cardiovascular system; endocrine system;

XX KW neurological system; forensic testing; paternity testing; PCR primer; ss.

XX OS Homo sapiens.

XX PN WO200058519-A2.

XX PD 05-OCT-2000.

XX PF 30-MAR-2000; 2000MO-US008440.

XX PR 31-MAR-1999; 99US-0127248P.

XX PA (WHD) WHITEHEAD INST BIOMEDICAL RES.

XX PA (AFHY-) AFFMETRIX INC.

XX PI Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;

XX PI Lipshutz RJ, Petzl N, Sklar P;

XX DR WPI; 2000-611722/58.

XX PT Nucleic acid selected from one of 106 genes comprising single nucleotide

PT polymorphisms, allele-specific oligonucleotides to the genes are useful

PT for phenotypic correlations, forensics, paternity testing, medicine and

PT genetic analysis.

XX Claim 8; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single

CC nucleotide polymorphisms (SNPs) which the inventors identified in human

CC genes. These SNPs can be used in disease diagnosis and prediction of an

CC individual's susceptibility to disease, in forensic and paternity testing

CC and in genetic mapping. In particular, the SNPs of the invention can be

CC used to diagnose susceptibility to diseases of the cardiovascular,

CC endocrine and neurological systems, such as coronary artery disease,

CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's

CC diseases

XX SQ Sequence 19 BP; 4 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

PN WO200168853-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-US007896.
 XX
 PR 14-MAR-2000; 2000US-0189226P.
 PR 28-DEC-2000; 2000US-0258452P.
 XX
 PA (UYUO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 PI Roden R, Naora H;
 XX
 XX WPI; 2001-596909/67.
 DR
 XX
 PT Novel cancer-related antigen useful for prognosis, diagnosis and
 PT treatment of cancer, especially ovarian cancer in an individual,
 PT comprises a fragment isolated from bacteriophage lambda.
 PS
 PS Example 5; Page 40; 67pp; English.
 XX
 XX The patent discloses autoantibodies in cancer patients specific for novel
 CC cancer-related antigens that are normally intracellular including for
 CC homeobox proteins, HoxA7, HoxB7, ADP ribosylation factor 1 (Arf-1), ATP
 CC dependent iron transporter ABC-7 and a novel protein encoded by
 CC SCOR1/Xho1 fragment isolated from bacteriophage lambda clone 44B.1. The
 CC presence of these autoantibodies is correlated with neoplastic processes
 CC in patients. Proteins of the invention are useful for screening for
 CC cancer in an individual. HoxB7 is useful for screening for cancer other
 CC than breast cancer, renal cell carcinoma, colon cancer or melanoma in an
 CC individual, by determining whether cells in the individual are expressing
 CC a gene product of HoxB7, expression of which is correlated with increased
 CC likelihood of cancer in the individual. It is useful for screening
 CC ovarian cancer or benign serous cystadenoma. HoxB7 proteins are useful to
 CC distinguish between neoplastic and non-neoplastic fluid accumulations in
 CC patients carrying a malignant diagnosis and in screening methods for
 CC therapeutically active materials. HoxB7 antibodies are useful for
 CC detecting epitopes found on proteins of the invention in histological
 CC sections of ovarian cancer tissue as well as in other solid tumours such
 CC as breast cancer and melanoma. The proteins of the invention are also
 CC used as vaccines. The present DNA sequence is a PCR primer which is used
 CC for amplifying human beta-actin DNA
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 317 TGAAGATCTTCA 328
 |||||
 |||||
 DB 8 TGAAGATCTTCA 19

PF 01-MAR-2000; 2000GB-00005005.
 XX
 PR 01-MAR-2000; 2000GB-00005005.
 XX
 PA (NOVS) NOVARTIS RES FOUND.
 XX
 PI Dumas F, Van Gelder P, Duckely M, Hohn B;
 XX
 XX WPI; 2001-618844/72.
 DR
 XX
 PT Delivering a material across a membrane, useful for producing transiently
 PT or stably transfected or transformed cells, comprises introducing
 PT Agrobacterium VirE2 into a membrane, where VirE2 forms a channel through
 PT the membrane.
 XX
 PS Example 1; Page 21; 30pp; English.
 XX
 XX The invention relates to a method of delivering a material across a
 CC membrane. The method involves introducing Agrobacterium VirE2, its
 CC fragment or homologue into a membrane, where VirE2, its fragment or
 CC homologue forms a channel through the membrane; contacting the membrane
 CC with a molecule desired to be transferred across the membrane; and
 CC allowing the molecule to cross the membrane through the channel. The
 CC method is useful in delivering materials across membranes, particularly
 CC into cells or organelles, and subsequently producing transiently or
 CC stably transfected or transformed cells. The method is especially useful
 CC for delivering nucleic acid to a cell to achieve expression of a desired
 CC transgene by the cell, and for treating cancer cells, relying on a new
 CC non-viral system without ITR and the possible hazards connected with
 CC them. The present sequence represents a VirE2 specific oligo used in the
 CC method of the invention
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 7 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 TTGATGACCGG 24
 |||||
 |||||
 DB 3 TTGATGACCGG 14

RESULT 228
 AAF84826
 ID AAF84826 standard; cDNA; 19 BP.
 XX
 AC AAF84826;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE PCR primer used for RACE-PCR reactions of human SPG4 cDNA.
 XX
 XX Human; SPG4 gene; spactin; PSF-AD; gene therapy; probe;
 KW autosomal dominant familial spastic paraplegia; PCR primer; ss.
 OS Homo sapiens.
 XX
 XX FR2798138-A1.
 XX
 PD 09-MAR-2001.
 XX
 PF 03-SEP-1999; 99FR-00011097.
 XX
 PR 03-SEP-1999; 99FR-00011097.
 PR (CNRS) CNRS CENT NAT RECH SCI.
 PA
 PI Weissenbach J, Hazan J;
 XX
 XX WPI; 2001-283966/30.
 DR
 XX
 PT New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of

RESULT 227
 ABL58227
 ID ABL58227 standard; DNA; 19 BP.
 XX
 AC ABL58227;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE A. tumefaciens VirE2 DNA specific oligonucleotide.
 XX
 KW VirE2; cytosolic; gene therapy; transfection; transformation;
 KM virulence protein; ss.
 OS Agrobacterium tumefaciens.
 XX
 XX GB2359812-A.
 XX
 PN
 PD 05-SEP-2001.
 XX

PT autosomal dominant familial spastic paraplegia and in drug screening.
XX
PS Claim 5; Page 24; 145pp; French.
XX
CC PCR primers AB84902-27 were used in RACE-PCR reactions of human SPG4
CC gene cDNA. The primers may also be used as probes. The SPG4 gene encodes
CC a spastin polypeptide. Mutations in the SPG4 gene are responsible for
CC autosomal dominant familial spastic paraplegia. SPG4 polynucleotides, and
CC their fragments, are used to screen DNA banks for sequences that encode
CC spastin (particularly sequences in other mammals, specifically mice); to
CC identify SPG4 mutations, or other genetic anomalies, particularly for
CC diagnosis of autosomal dominant familial spastic paraplegia (PSF-AD); to
CC identify promoters and other regulatory elements of the SPG4 gene; for
CC detection and amplification; for recombinant production of spastin; and
CC for diagnostic genotyping of PSF-AD
XX
SQ Sequence 19 BP; 4 A; 5 C; 3 G; 7 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 441 CTGGAATCTTT 452
DB 1 CTGGAATCTTT 12

RESULT 229
ABK89543/c
ID ABK89543 standard; DNA; 19 BP.
XX
AC ABK89543;
XX
DT 21-OCT-2002 (first entry)
XX
DE Synthetic PCR primer Acctf.
XX
KM Barley yellow dwarf virus infection; BYDV; plant resistance;
KM monocotyledon; wheat; Triticum; Sorghum; rice; Oryza; barley; Hordeum;
KM maize; Zea; Tye; Secale; triticales; oat; Avena; antiviral; gene therapy;
KM PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO200248394-A1.
XX
PD 20-JUN-2002.
XX
PF 13-DEC-2001; 2001WO-AU001611.
XX
PR 15-DEC-2000; 2000AU-00002103.
XX
PR 21-MAY-2001; 2001US-0292778P.
XX
PA (GRAI-) GRAIN BIOTECHNOLOGY AUSTRALIA PTY LTD.
XX
PI Bower R, Lehto K, Junttila TT, Yang R, Pehu E;
XX
PI WPI; 2002-563533/62.
XX
DR
XX
PT Protecting plant from barley yellow dwarf virus infection, by
PT transforming modified nucleic acid expressing translationally-altered RNA
PT into a plant cell, which confers resistance against virus infection.
XX
PS Example 9; Page 60; 89pp; English.
XX
CC The present invention relates to a new method of protecting a plant from
CC barley yellow dwarf virus (BYDV) infection. The method of the invention
CC comprises transforming a modified nucleic acid molecule into a plant
CC cell, where the expression of the nucleic acid molecule results in the
CC expression of a translationally-altered RNA molecule which confers to the
CC plant resistance against infection with BYDV. The method is useful for
CC protecting a plant from BYDV infection, where the plant is a
CC monocotyledon selected from wheat (Triticum), sorghum (Sorghum), rice

CC (Oryza), barley (Hordeum), maize (Zea), rye (Secale), triticales and oat
CC (Avena), preferably wheat. The present nucleic acid sequence represents a
CC synthetic PCR primer that was used in the methods of the invention
XX
SQ Sequence 19 BP; 6 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 317 TGAGATCTTCA 328
DB 18 TGAGATCTTCA 7

RESULT 230
ADA03189
ID ADA03189 standard; DNA; 19 BP.
XX
AC ADA03189;
XX
DT 06-NOV-2003 (first entry)
XX
DE Wild type sequence in human p53 around position R249S in mutant gene.
XX
KM cytosolic; virucide; anti-HIV; neuroprotective; ophthalmological;
KM antidiabetic; antipsoriatic; antirheumatic; antiarthritic; ds;
KM inhibitor repression; inhibitor RNA; apoptosis; necrosis;
KM differentiation; tumour cell division; BCL2 gene family;
KM matrix metalloproteinase; membrane metalloproteinase;
KM nuclear hormone receptor; transcription factor;
KM vascular endothelial growth factor; p53; chromosomal translocation;
KM leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;
KM AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;
KM psoriasis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN WO2003040366-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-FR003843.
XX
PR 09-NOV-2001; 2001FR-00014549.
XX
PR 10-APR-2002; 2002FR-00004474.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Harel-Bellan A, Alt-St-Alt S, Cabon-Georget F, Chauchereau A;
PI Dautry F;
XX
XX
XX WPI; 2003-441571/41.
XX
PT New double-stranded oligonucleotides, useful e.g. for treatment and
PT diagnosis of tumors, comprise complementary strands with single-stranded
PT overhangs.
XX
PS Disclosure; Page 17; 148pp; French.
XX
CC The invention relates to double-stranded oligonucleotides consisting of
CC two complementary strands (1a; 1b), each having 1-5 unpaired nucleotides,
CC at either at their 3' and 5' ends, forming single-stranded overhangs. One
CC of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),
CC that is to be specifically repressed. The oligonucleotides are preferably
CC double stranded inhibitor RNA molecules with a couple of thymidine bases
CC attached at the 3' or 5' ends. The targets are preferably nucleic acids
CC that, when repressed, induce apoptosis, necrosis or differentiation of
CC tumour cells and/or inhibit division of such cells. Typical of many
CC specified targets include: genes of the BCL2 family; genes that encode
CC metalloproteases (matrix or membrane) or their inhibitors; genes encoding
CC mutant forms of nuclear hormone receptors; a sequence encoding the Hsp-
CC alpha transcription factor; sequences encoding various isoforms of the

CC vascular endothelial growth factor; viral genes; genes that express a
 CC mutated protein, e.g. inactive p53; genes that are formed by a
 CC chromosomal translocation, e.g. where associated with leukaemia, and
 CC genes that express androgen receptors. The oligonucleotides are used: (1)
 CC to study gene function; (ii) for therapy or diagnosis, particularly of
 CC conditions caused by expression of a harmful gene or fusion protein.
 CC specifically cancer (e.g. associated with expression of mutant p53 or of
 CC the human papilloma virus B6 protein), viral infections, especially AIDS
 CC or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD
 CC ; and (iii) for treating hypervascular diseases, e.g. age-related macular
 CC degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis
 CC and rheumatoid arthritis. They may also be used in vitro, e.g. for
 CC treating transplants and for establishing a genetic profile, for
 CC individualization, or modification, of treatment regimes. They provide
 CC very effective and very specific repression of genes. RNA hybrids are
 CC more stable than either hybrids prepared from DNA or single-stranded
 CC sequences; contain only natural components (so will not induce
 CC immunological or intolerance reactions) and they enter tumour cells more
 CC effectively than plasmids. This sequence represents the sequence in the
 CC wild type human p53 gene around the position of mutation R249S. The
 CC oligonucleotides of the invention can be targeted to this sequence.

SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ATGACC GGAGG 27
 |||||
 Db 3 ATGACC GGAGG 14

RESULT 231
 ADA03188
 ID ADA03188 standard; DNA; 19 BP.
 XX
 AC ADA03188;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Wild type sequence in human p53 around position R248W in mutant gene.
 XX
 KW cytostatic; virocidic; anti-HIV; neuroprotective; ophthalmological;
 KW antidiabetic; antipsoriatic; antirheumatic; antiarthritic; de;
 KW inhibitor repression; inhibitor RNA; apoptosis; necrosis;
 KW differentiation; tumour cell division; BCL2 gene family;
 KW matrix metalloprotease; membrane metalloprotease;
 KW nuclear hormone receptor; transcription factor;
 KW vascular endothelial growth factor; p53; chromosomal translocation;
 KW leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;
 KW AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;
 KW psoriasis; rheumatoid arthritis.

XX
 OS Homo sapiens.
 XX
 PN MO2003040366-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 08-NOV-2002; 2002WO-FR003843.
 XX
 PR 09-NOV-2001; 2001FR-00014549.
 XX
 PR 10-APR-2002; 2002FR-00004474.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Harel-Bellan A, Alt-St-Ali S, Cabon-Georget F, Chacheureau A;
 XX Dautry F,
 DR WPI, 2003-441571/41.
 XX
 PT New double-stranded oligonucleotides, useful e.g. for treatment and

PT diagnosis of tumors, comprise complementary strands with single-stranded
 PT overhangs.

XX Disclosure; Page 17; 148pp; French.

PS The invention relates to double-stranded oligonucleotides consisting of
 CC two complementary strands (1a, 1b), each having 1-5 unpaired nucleotides,
 CC at either at their 3' and 5' ends, forming single-stranded overhangs. One
 CC of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),
 CC that is to be specifically repressed. The oligonucleotides are preferably
 CC double stranded inhibitor RNA molecules with a couple of thymidine bases
 CC attached at the 3' or 5' ends. The targets are preferably nucleic acids
 CC that, when repressed, induce apoptosis, necrosis or differentiation of
 CC tumour cells and/or inhibit division of such cells. Typical of many
 CC specified targets include: genes of the BCL2 family; genes that encode
 CC metalloproteases (matrix or membrane) or their inhibitors; genes encoding
 CC mutant forms of nuclear hormone receptors; a sequence encoding the Hfl-
 CC alpha transcription factor; sequences encoding various isoforms of the
 CC vascular endothelial growth factor; viral genes; genes that express a
 CC mutated protein, e.g. inactive p53; genes that are formed by a
 CC chromosomal translocation, e.g. where associated with leukaemia, and
 CC genes that express androgen receptors. The oligonucleotides are used: (i)
 CC to study gene function; (ii) for therapy or diagnosis, particularly of
 CC conditions caused by expression of a harmful gene or fusion protein,
 CC specifically cancer (e.g. associated with expression of mutant p53 or of
 CC the human papilloma virus B6 protein), viral infections, especially AIDS
 CC or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD
 CC ; and (iii) for treating hypervascular diseases, e.g. age-related macular
 CC degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis
 CC and rheumatoid arthritis. They may also be used in vitro, e.g. for
 CC treating transplants and for establishing a genetic profile, for
 CC individualization, or modification, of treatment regimes. They provide
 CC very effective and very specific repression of genes. RNA hybrids are
 CC more stable than either hybrids prepared from DNA or single-stranded
 CC sequences; contain only natural components (so will not induce
 CC immunological or intolerance reactions) and they enter tumour cells more
 CC effectively than plasmids. This sequence represents the sequence in the
 CC wild type human p53 gene around the position of mutation R248W. The
 CC oligonucleotides of the invention can be targeted to this sequence.

SQ Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 ATGACC GGAGG 27
 |||||
 Db 3 ATGACC GGAGG 14

RESULT 232
 ADA03187
 ID ADA03187 standard; DNA; 19 BP.
 XX
 AC ADA03187;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Wild type sequence in human p53 around position R248Q in mutant gene.
 XX
 KW cytostatic; virocidic; anti-HIV; neuroprotective; ophthalmological;
 KW antidiabetic; antipsoriatic; antirheumatic; antiarthritic; de;
 KW inhibitor repression; inhibitor RNA; apoptosis; necrosis;
 KW differentiation; tumour cell division; BCL2 gene family;
 KW matrix metalloprotease; membrane metalloprotease;
 KW nuclear hormone receptor; transcription factor;
 KW vascular endothelial growth factor; p53; chromosomal translocation;
 KW leukaemia; androgen receptor; diagnosis; cancer; human papilloma virus;
 KW AIDS; BSE; CJD; macular degeneration; angiogenesis; diabetic retinopathy;
 KW psoriasis; rheumatoid arthritis.

XX
 OS Homo sapiens.

XX WO2003040366-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 08-NOV-2002; 2002WO-FR003843.
 XX
 XX 09-NOV-2001; 2001FR-00014549.
 XX 10-APR-2002; 2002FR-00004474.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Harel-Bellan A, Ait-Si-All S, Cabon-Georget F, Chauchereau A,
 XX Daury F;
 XX WPI; 2003-441571/41.
 XX
 XX New double-stranded oligonucleotides, useful e.g. for treatment and
 XX diagnosis of tumors, comprise complementary strands with single-stranded
 XX overhangs.
 XX
 XX Disclosure; Page 17; 148pp; French.
 XX
 XX The invention relates to double-stranded oligonucleotides consisting of
 XX two complementary strands (1a; 1b), each having 1-5 unpaired nucleotides,
 XX at either at their 3' and 5' ends, forming single-stranded overhangs. One
 XX of (1a) and (1b) is complementary to a target sequence, (DNA or RNA),
 XX that is to be specifically repressed. The oligonucleotides are preferably
 XX double stranded inhibitor RNA molecules with a couple of thymidine bases
 XX attached at the 3' or 5' ends. The targets are preferably nucleic acids
 XX that, when repressed, induce apoptosis, necrosis or differentiation of
 XX tumour cells and/or inhibit division of such cells. Typical of many
 XX specified targets include: genes of the BCL2 family; genes that encode
 XX metalloproteases (matrix or membrane) or their inhibitors; genes encoding
 XX mutant forms of nuclear hormone receptors; a sequence encoding the Hfl-
 XX alpha transcription factor; sequences encoding various isoforms of the
 XX vascular endothelial growth factor; viral genes; genes that express a
 XX mutated protein, e.g. inactive p53; genes that are formed by a
 XX chromosomal translocation, e.g. where associated with leukemia, and
 XX genes that express androgen receptors. The oligonucleotides are used: (1)
 XX to study gene function; (ii) for therapy or diagnosis, particularly of
 XX conditions caused by expression of a harmful gene or fusion protein,
 XX specifically cancer (e.g. associated with expression of mutant p53 or of
 XX the human papilloma virus E6 protein), viral infections, especially AIDS
 XX or cancer-inducing viruses, or unconventional infections, e.g. BSE or CJD
 XX ; and (iii) for treating hypervascular diseases, e.g. age-related macular
 XX degeneration, angiogenesis in tumours, diabetic retinopathy, psoriasis
 XX and rheumatoid arthritis. They may also be used in vitro, e.g. for
 XX treating transplants and for establishing a genetic profile, for
 XX individualization, or modification, of treatment regimes. They provide
 XX very effective and very specific repression of genes. RNA hybrids are
 XX more stable than either hybrids prepared from DNA or single-stranded
 XX sequences; contain only natural components (so will not induce
 XX immunological or intolerance reactions) and they enter tumour cells more
 XX effectively than plasmids. This sequence represents the sequence in the
 XX wild type human p53 gene around the position of mutation R248Q. The
 XX oligonucleotides of the invention can be targeted to this sequence.
 XX
 XX Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 7; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 16 ATGAACCGGAGG 27
 XX |||||
 XX 3 ATGAACCGGAGG 14
 XX
 XX RESULT 233
 XX ADB54361/c
 XX ID ADB54361 standard; DNA; 19 BP.
 XX

AC ADB54361;
 XX
 XX 04-DEC-2003 (first entry)
 XX
 XX PCR primer 29 used to amplify genomic DNA region.
 XX
 XX colon cell proliferative disorder; non methylated CpG dinucleotide;
 XX cytosinetic; cancer; adenoma; carcinoma; cytosine methylation state; ss;
 XX PCR; primer.
 XX
 XX Unidentified.
 XX
 XX WO2003072821-A2.
 XX
 XX 04-SEP-2003.
 XX
 XX 27-FEB-2003; 2003WO-EP002035.
 XX
 XX 27-FEB-2002; 2002EP-00004551.
 XX
 XX (EPIC-) EPIDEMIOLOGICS AG.
 XX
 XX Adorian P, Burger M, Maier S, Nimmrich I, Becker E, Lesche R,
 XX Rujan T, Schmitt A;
 XX WPI; 2003-731620/69.
 XX
 XX Detecting and differentiating between colon cell proliferative disorders
 XX associated with a gene or its regulatory regions comprises contacting a
 XX target nucleic acid in a biological sample obtained from the subject with
 XX a reagent.
 XX
 XX Claim 15; Page 22; 74pp; English.
 XX
 XX The invention relates to a novel method for detecting and differentiating
 XX between colon cell proliferative disorders associated with at least one
 XX gene or its regulatory regions. The method comprises contacting a target
 XX nucleic acid in a biological sample obtained from the subject with at
 XX least one reagent or a series of reagents, where the reagent or series of
 XX reagents, distinguishes between methylated and non methylated CpG
 XX dinucleotides within the target nucleic acid. The molecules of the
 XX invention demonstrate cytosinetic activity whilst the method may be useful
 XX for detecting and differentiating between colon cell proliferative
 XX disorders, including cancers such as colon adenoma and colon carcinoma.
 XX The RNA (peptide nucleic acid)-oligomers are useful as probes for
 XX determining cytosine methylation state or single nucleotide
 XX polymorphisms. The current sequence is that of the PCR primer of the
 XX invention which was used to amplify the genomic DNA region.
 XX
 XX Sequence 19 BP; 4 A; 0 C; 10 G; 5 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 9; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 301 AACCCCAACCTC 312
 XX |||||
 XX 12 AACCCCAACCTC 1
 XX
 XX RESULT 234
 XX ADE29549/c
 XX ID ADE29549 standard; RNA; 19 BP.
 XX
 XX ADE29549;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 XX Mitogen activated protein kinase siRNA oligonucleotide SEQ ID NO:171.
 XX
 XX short interfering nucleic acid; siRNA; downregulation; inhibition;
 XX mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 XX cytosinetic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 XX

KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 OS Synthetic.
 PN WO2003072590-A1.
 PD 04-SEP-2003.
 PF 28-JAN-2003; 2003WO-US002510.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA Mcswigen J, Beigelman L, Usman N, Haeblerli P, Chowrira B;
 PI WPI; 2003-689980/65.
 DR New short interfering nucleic acid, useful e.g. for treatment and
 XX diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 PS Example 3; SEQ ID NO 171; 164pp; English.
 XX The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antilasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiallergic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.
 SO Sequence 19 BP; 1 A; 10 C; 7 G; 0 T; 1 U; 0 Other;
 QY Query Match 2.0%; Score 12; DB 9; Length 19;
 Db Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 381 GCGGCTGCACCG 392
 19 GCGGCTGCACCG 8
 RESULT 235
 ADE29386
 ID ADE29386 standard; RNA; 19 BP.
 AC ADE29386;
 XX
 DT 29-JAN-2004 (first entry)
 XX

DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:8.
 XX short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytostatic; anorectic; antidiabetic; antiinflammatory; antilasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 OS Synthetic.
 PN WO2003072590-A1.
 PD 04-SEP-2003.
 PF 28-JAN-2003; 2003WO-US002510.
 PR 20-FEB-2002; 2002US-0358580P.
 PR 11-MAR-2002; 2002US-0363124P.
 PR 06-JUN-2002; 2002US-0386782P.
 PR 29-AUG-2002; 2002US-0406784P.
 PR 05-SEP-2002; 2002US-0408378P.
 PR 09-SEP-2002; 2002US-0409293P.
 PR 15-JAN-2003; 2003US-0440129P.
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA Mcswigen J, Beigelman L, Usman N, Haeblerli P, Chowrira B;
 PI WPI; 2003-689980/65.
 DR New short interfering nucleic acid, useful e.g. for treatment and
 XX diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 PS Example 3; SEQ ID NO 8; 164pp; English.
 XX The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antilasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiallergic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes, in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.
 SO Sequence 19 BP; 1 A; 7 C; 10 G; 0 T; 1 U; 0 Other;
 QY Query Match 2.0%; Score 12; DB 9; Length 19;
 Db Best Local Similarity 91.7%; Pred. No. 1.2e+05;
 Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 381 GCGGCTGCACCG 392
 1 GCGGCTGCACCG 12
 RESULT 236
 AA052874
 ID AA052874 standard; RNA; 20 BP.

XX AC AAQ52874;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-MAY-1994 (first entry)
 XX
 DE Cytomegalovirus target sequence 51.
 XX
 KM RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; hnRNA;
 KM picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV;
 KM papilloma virus; HPV; Epstein-Barr virus; EBV; TGLV;
 KM T-cell leukemia virus; hepatitis C virus; HCV; cytomegalovirus;
 KM influenza virus; HSV; herpes simplex virus; vector; immune response;
 KM antibody; ribozyme; viral RNA; treatment; ss.
 XX
 OS Synthetic.
 XX
 PN WO9323569-A1.
 XX
 PD 25-NOV-1993.
 XX
 PF 29-APR-1993; 93MO-US004020.
 XX
 PR 11-MAY-1992; 92US-00882689.
 PR 14-MAY-1992; 92US-00882712.
 PR 14-MAY-1992; 92US-00882713.
 PR 14-MAY-1992; 92US-00882714.
 PR 14-MAY-1992; 92US-00882823.
 PR 14-MAY-1992; 92US-00882824.
 PR 14-MAY-1992; 92US-00882885.
 PR 14-MAY-1992; 92US-00882886.
 PR 14-MAY-1992; 92US-00882889.
 PR 14-MAY-1992; 92US-00882921.
 PR 14-MAY-1992; 92US-00882922.
 PR 14-MAY-1992; 92US-00883823.
 PR 14-MAY-1992; 92US-00883849.
 PR 14-MAY-1992; 92US-00884073.
 PR 14-MAY-1992; 92US-00884074.
 PR 14-MAY-1992; 92US-00884333.
 PR 14-MAY-1992; 92US-00884422.
 PR 14-MAY-1992; 92US-00884431.
 PR 14-MAY-1992; 92US-00884436.
 PR 14-MAY-1992; 92US-00884521.
 PR 31-JUL-1992; 92US-00923738.
 PR 26-AUG-1992; 92US-00935854.
 PR 18-SEP-1992; 92US-00948355.
 PR 15-OCT-1992; 92US-00963322.
 PR 07-DEC-1992; 92US-00987129.
 PR 07-DEC-1992; 92US-00987130.
 PR 07-DEC-1992; 92US-00987133.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Draper KG, Dudycz LW, Mcswiggen JA, Macejak DG, Holecsek JJ;
 PI Mamone JA;
 XX
 DR WPI; 1993-386599/48.
 XX
 PT Enzymatic RNA molecules - used to inhibit viral replication, infection
 PT and gene expression.
 XX
 PS Claim 5; Fig 13; 287bp; English.
 XX
 CC The sequences (AAQ52824-Q52890) are pref. Cytomegalovirus target
 CC sequences for enzymatic RNA molecules. The RNA molecules are
 CC complementary to a substrate binding region in the specified gene target.
 CC They also have enzymatic activity in that they specifically cleave RNA
 CC in the target. The RMs interfere with viral replication and therefore
 CC have anti-viral properties. They can be used to attenuate viruses to be
 CC used in vaccines. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)

XX SQ Sequence 20 BP; 1 A; 9 C; 5 G; 0 T; 5 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1,2e+05;
 Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 223 TGCTACCGCGTC 234
 DB 4 UGCUACCGCGTC 15
 XX
 RESULT 237
 ID AAQ55841 standard; DNA; 20 BP.
 XX
 AC AAQ55841;
 XX
 DT 21-JUL-1994 (first entry)
 XX
 DE HCV detection primer (DNA type 5 S67).
 XX
 KM HCV; hepatitis C virus; detection; primer; PCR; mixer primer set;
 KM polymerase chain reaction; DNA polymerase; ss.
 XX
 OS Synthetic.
 XX
 PN JP05337000-A.
 XX
 PD 21-DEC-1993.
 XX
 PF 04-JUN-1992; 92JP-00168226.
 XX
 PR 04-JUN-1992; 92JP-00168226.
 XX
 PA (SAYA/) SAYAMA K.
 XX
 DR WPI; 1994-037380/05.
 XX
 PT Detection of type C hepatitis virus - using one step DNA polymerase chain
 PT reaction with mixed primer set.
 XX
 PS Claim 2; Page 2; 7bp; Japanese.
 XX
 CC The primers (AAQ55811-841) are used to detect various types of hepatitis
 CC C virus. The primers are made from oligo DNA fragments selected from
 CC specific hepatitis C virus subtypes. The primers can be used to in a one
 CC step PCR reaction which can determine the subtypes of a large number of
 CC samples
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
 XX
 Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1,2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 36 TTACCAATTCAA 47
 DB 8 TTACCAATTCAA 19
 XX
 RESULT 238
 ID AAQ94258/c standard; DNA; 20 BP.
 XX
 AC AAQ94258;
 XX
 DT 05-DEC-1995 (first entry)
 XX
 DE Antisense primer to amplify 429 bp SV40 large T antigen gene fragment.
 XX
 KM primer; PCR; polymerase chain reaction; SV40; large T antigen;
 KM mouse hepatoma cell; animal model; cancer; ss.

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XX OS Synthetic.
XX PS JP07079773-A.
XX PD 28-MAR-1995.
XX PF 19-JUL-1994; 94JP-00166647.
XX PR 20-JUL-1993; 93JP-00179402.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX DR WPI; 1995-157844/21.
XX PT Mouse hepatoma cell line - useful in animal model systems of cancer.
XX PS Example; Page 4; 5pp; Japanese.
XX CC This antisense primer was used in PCR, with the sense primer shown in
CC AAQ94257, to amplify a region from nucleotides 1571 to 2009 of the SV40
CC large T antigen gene. A fragment of 429 bp was generated. The fragment is
CC used in the invention, a mouse hepatoma cell line which may metastasise
CC specifically in the liver and contains an albumin promoter gene and a
CC SV40-T gene. The cell line is useful for the production of animal models
CC for the study of cancer and screening of anti-cancer agents
XX SQ Sequence 20 BP; 5 A; 2 C; 4 G; 9 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 423 CAAGATATTT 434
   |||||
Db 18 CAAGATATTT 7

RESULT 239
AAQ91041/c
ID AAQ91041 standard; DNA; 20 BP.
XX AC AAQ91041;
XX DT 30-JAN-1996 (first entry)
XX DE HHV-6 associated MS genetic marker MDP internal primer MSHind9.
XX KM Human herpes virus-6; HHV-6; multiple sclerosis; genetic marker; MDP;
XX KW internal primer MSHind9; diagnosis; ss.
XX OS Synthetic.
XX PN WO9512313-A1.
XX PD 11-MAY-1995.
XX PF 04-NOV-1994; 94WO-US012655.
XX PR 05-NOV-1993; 93US-00149176.
XX PR 24-MAR-1994; 94US-00218029.
XX PR 05-AUG-1994; 94US-00287942.
XX PR 04-NOV-1994; 94US-00334482.
XX PA (PATH-) PATHOGENESIS CORP.
XX PI Burner GC, Chailoner PB, Smith KT, Brown JP, Parker JD;
XX PI Nowinski RC;
XX DR WPI; 1995-215032/28.
XX PT Treatment of human herpes-virus-6-associated multiple sclerosis - using
XX an antiviral agent, e.g. a nucleoside analogue, administered to the

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PT cerebrospinal fluid.
XX PS Disclosure; Page 34; 11pp; English.
XX PD AAQ91041 and AAQ91042 are an internal primer pair for the human herpes
XX virus-6 (HHV-6) associated multiple sclerosis (MS) genetic marker, MDP
XX CC (AAQ91043). The primers can be used in the diagnosis of MS
XX SQ Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

Query Match      2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 TCGGCGTGAGAC 80
   |||||
Db 17 TCGGCGTGAGAC 6

RESULT 240
AAT08653/c
ID AAT08653 standard; DNA; 20 BP.
XX AC AAT08653;
XX DT 05-SEP-1996 (first entry)
XX DE Primer p53-5X6p for p53 gene exon 6 amplification.
XX KM primer; PCR; polymerase chain reaction; hierarchy; immunoassay;
XX KW quantitative assay; fragment length; DNA sequencing; p53; mutation; ss.
XX OS Synthetic.
XX PN WO9601909-A1.
XX PD 25-JAN-1996.
XX PF 07-JUL-1995; 95WO-US008605.
XX PR 08-JUL-1994; 94US-00271946.
XX PR 14-FEB-1995; 95US-00388381.
XX PA (VISI-) VISIBLE GENETICS INC.
XX PI Diamandis E, Dunn JM, Stevens JK;
XX DR WPI; 1996-097638/10.
XX PT Testing for disease-associated p53 gene mutation(s) using a hierarchy of
XX PT assay techniques - e.g. immunoassay, DNA amplification and DNA
XX PT sequencing.
XX PS Claim 18; Page 21; 44pp; English.
XX SQ Rapid and cost effective diagnosis of disease-associated mutations in the
XX p53 gene is achieved by employing a selected number of diagnostic tools,
XX in a hierarchy of increasing accuracy and cost per tool, in which each
XX tool detects essentially no false positives. Tests that may be employed,
XX in order of increasing accuracy and cost are: (a) immunoassays; (b) DNA
XX fragment length/quantity analysis; and (c) DNA sequencing of regions
XX most likely to harbour point mutations. AAT08645-66 are primers used in
XX DNA fragment length/quantity analysis. The amplification of the eleven
XX exons is advantageously carried out in 3 multiplex pools, the members of
XX a pool selected because they all use the same hybridisation temperature
XX and none of the expected fragment lengths will overlap in an
XX electrophoresis gel. One of each pair of primers is labeled at the 5' end
XX with an identifiable marker such as fluorescein, rhodamine or cyanine.
XX The present sequence is used with AAT08654 to amplify a 247 bp fragment
XX of exon 6
XX SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

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Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
 |||||
 DB 18 TCGTCTCTCCAG 7

RESULT 241

AA08652
 ID AA08652 standard; DNA; 20 BP.

AC AA08652;

DT 05-SEP-1996 (first entry)

DE Primer P53-3X5MP for p53 gene exon 5 amplification.

KM primer; PCR; polymerase chain reaction; hierarchy; immunoassay;

KM quantitative assay; fragment length; DNA sequencing; p53; mutation; ss.

OS Synthetic.

PN MO9601909-A1.

PD 25-JAN-1996.

PF 07-JUL-1995; 95WO-US008605.

PR 08-JUL-1994; 94US-00271946.

PR 14-FEB-1995; 95US-00386381.

PA (VISI-) VISIBLE GENETICS INC.

PI Diamandis E, Dunn JM, Stevens JK.

DR WPI; 1996-097638/10.

PT Testing for disease-associated p53 gene mutation(s) using a hierarchy of
 assay techniques - e.g. immunoassay, DNA amplification and DNA
 sequencing.

PS Claim 18; Page 21; 44pp; English.

XX Rapid and cost effective diagnosis of disease-associated mutations in the
 CC p53 gene is achieved by employing a selected number of diagnostic tools,
 CC in a hierarchy of increasing accuracy and cost per tool, in which each
 CC tool detects essentially no false positives. Tests that may be employed,
 CC in order of increasing accuracy and cost are: (a) immunoassays; (b) DNA
 CC fragment length/quantity analysis; and (c) DNA sequencing of regions
 CC most likely to harbour point mutations. AA08645-66 are primers used in
 CC DNA fragment length/quantity analysis. The amplification of the eleven
 CC exons is advantageously carried out in 3 multiplex pools, the members of
 CC a pool selected because they all use the same hybridisation temperature
 CC and none of the expected fragment lengths will overlap in an
 CC electrophoresis gel. One of each pair of primers is labeled at the 5' end
 CC with an identifiable marker such as fluorescein, rhodamine or cyanine.
 CC The present sequence is used with AA08651 to amplify a 268 bp fragment
 CC of exon 5

XX Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
 |||||
 DB 9 TCGTCTCTCCAG 20

RESULT 242

AA09864/C
 ID AA09864 standard; DNA; 20 BP.

AC AA09864;

DT 07-MAY-1998 (first entry)

DE Primer for exon 6 of p53 gene.

KM PCR primer; amplify; pathogen identification; mutation detection;

KM nucleic acid analysis; microorganism characterisation; human;

KM HLA type determination; p53 gene exon 6; ss.

OS Synthetic.

PN MO9741259-A1.

PD 06-NOV-1997.

PF 29-APR-1997; 97WO-US007135.

PR 01-MAY-1996; 96US-00640672.

PR 19-JUL-1996; 96US-00684498.

PR 27-FEB-1997; 97US-00807138.

PA (VISI-) VISIBLE GENETICS INC.

PI Leishner J, Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R;

DR WPI; 1997-549755/50.

PT Nucleic acid sequence determination - comprising synthesising chain
 extension products, which are indicative of positions of selected species
 of nucleotide in nucleotide sequence.

PS Example 4; Page 19; 69pp; English.

XX This sequence represents a primer for exon 6 of the p53 gene. This
 CC sequence can be used in the method of the invention for determining the
 CC position of at least one selected species of nucleotide, in a region of
 CC interest, in a target nucleic acid polymer, in a sample. The method
 CC comprises combining the sample with a reaction mixture to synthesise
 CC chain extension products indicative of the positions of the species of
 CC nucleotide in the region of interest and evaluating the products
 CC produced, characterised in that the sample, which is combined with the
 CC reaction mixture, and contains target and non-target nucleic acid
 CC polymers in natural abundance. The method can be used to detect
 CC mutations, particularly mutations of medical significance, in samples
 CC derived from a human patient, animal, plant or microorganism, determine
 CC HLA type ancillary to transplant procedures, detect and identify
 CC microorganisms, particularly pathogenic microorganisms, in a sample and
 CC in situ sequencing reactions to produce sequencing fragments in a
 CC histological specimen

XX Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

QY Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
 |||||
 DB 18 TCGTCTCTCCAG 7

RESULT 243

AA09863
 ID AA09863 standard; DNA; 20 BP.

AC AA09863;

DT 07-MAY-1998 (first entry)

```

XX DE Primer for exon 5 of p53 gene.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9741259-A1.
XX PD 06-NOV-1997.
XX PF 29-APR-1997; 97WO-US007135.
XX PR 01-MAY-1996; 96US-00640672.
XX PR 19-JUL-1996; 96US-00684498.
XX PR 27-FEB-1997; 97US-00807138.
XX PA (VISI-) VISIBLE GENETICS INC.
XX PI Leusiner J, Hui M, Dunn JM, Larson MT, Lacroix J, Shipman R;
XX DR WPI; 1997-549755/50.
XX PT Nucleic acid sequence determination - comprising synthesising chain
XX PT extension products, which are indicative of positions of selected species
XX PT of nucleotide in nucleotide sequence.
XX PS Example 4; Page 19; 69pp; English.
XX CC This sequence represents a primer for exon 5 of the p53 gene. This
XX CC sequence can be used in the method of the invention for determining the
XX CC position of at least one selected species of nucleotide, in a region of
XX CC interest, in a target nucleic acid polymer, in a sample. The method
XX CC comprises combining the sample with a reaction mixture to synthesise
XX CC chain extension products indicative of the positions of the species of
XX CC nucleotide in the region of interest and evaluating the products
XX CC produced, characterised in that the sample, which is combined with the
XX CC reaction mixture, and contains target and non-target nucleic acid
XX CC polymers in natural abundance. The method can be used to detect
XX CC mutations, particularly mutations of medical significance, in samples
XX CC derived from a human patient, animal, plant or microorganism, determine
XX CC HLA type ancillary to transplant procedures, detect and identify
XX CC microorganisms, particularly pathogenic microorganisms, in a sample and
XX CC in situ sequencing reactions to produce sequencing fragments in a
XX CC histological specimen
XX SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 510 TCCTCTCTCCAG 521
XX DB 9 TCCTCTCTCCAG 20
XX
XX RESULT 244
XX ID AAT79479/c
XX AC AAT79479 standard; DNA; 20 BP.
XX AC AAT79479;
XX DT 22-OCT-1997 (first entry)
XX DE DNA ligand for adenosine or adenosine 5'-phosphate.
XX DE
XX DE Adenosine; adenosine-5'-phosphate; adenosine triphosphate; ATP; binding;
XX KM ligand; purification; reagent; isolation; determination;
XX KM subcellular localisation; catalyst; assay; SELEX;

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```

XX KM Systematic Evolution of Ligands by Exponential enrichment; ss.
XX OS Synthetic.
XX PN US631146-A.
XX PD 20-MAY-1997.
XX PF 19-JAN-1995; 95US-00375116.
XX PR 19-JAN-1995; 95US-00375116.
XX PA (GENO) GEN HOSPITAL CORP.
XX PI Szostak JM, Huizenga DE;
XX DR WPI; 1997-288574/26.
XX PT Single stranded DNA molecule, which binds adenosine or adenosine-5'-
XX PT phosphate - useful as purification reagent, or for determination of
XX PT adenosine triphosphate subcellular localisation in vivo.
XX PS Claim 3; Col 63-64; 55pp; English.
XX CC The present sequence is an adenosine or adenosine-5'-phosphate (ASP)
XX CC binding single stranded DNA molecule, which can be used as a purification
XX CC reagent for the isolation of adenosine or an ASP, or to determine the
XX CC subcellular localisation of, e.g. adenosine triphosphate (ATP), in vivo.
XX CC The DNA molecule was prepared by contacting DNA molecules having a region
XX CC of random sequence with adenosine or ASP (preferably ATP), isolating a
XX CC subpopulation by partitioning DNA molecules which specifically bind the
XX CC adenosine or ASP, amplifying the subpopulation in vitro and repeating the
XX CC process 4 times to obtain a single stranded DNA molecule capable of
XX CC binding adenosine or ASP, i.e. Systematic Evolution of Ligands by
XX CC Exponential enrichment (SELEX). Catalytic DNA produced using the method
XX CC can be used as in vitro or in vivo catalysts, or to detect the presence
XX CC of the ligand. They may also be used in assays to detect molecules
XX CC modified by the DNA, which are not themselves ligands, e.g. DNA
XX CC phosphorylated by a polynucleotide kinase catalyst. The DNA molecule has
XX CC significant advantages over ligand binding and catalytic RNA in terms of
XX CC stability and synthesis cost
XX SQ Sequence 20 BP; 7 A; 1 C; 7 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 180 CTTCCTCCGCTA 191
XX DB 16 CTTCCTCCGCTA 5
XX
XX RESULT 245
XX ID AAT91100
XX AC AAT91100 standard; DNA; 20 BP.
XX AC AAT91100;
XX DT 27-MAR-1998 (first entry)
XX DE Bovine lysosomal alpha-mannosidase (LAMAN) gene PCR primer mp5UTIF.
XX DE
XX DE LAMAN; lysosomal alpha-mannosidase; alpha-mannosidosis; cattle;
XX KM diagnosis; screening; genetic test; PCR; primer; RFLP;
XX KM restriction fragment length polymorphism; ss.
XX OS Synthetic.
XX OS Bos taurus.
XX PN WO9726369-A1.
XX PD 24-JUN-1997.

```

XX PF 15-JAN-1997; 97WO-GB000109.
 XX PR 15-JAN-1996; 96NO-00000163.
 XX PA (HEAL/) HEALY P.
 XX PA (DZIE/) DZIEGLEWSKA H.
 XX PI Berg T, Tollersrud OK, Nilsen O;
 XX DR WPI; 1997-385352/35.
 XX PT Diagnosis and screening for bovine alpha-mannosidosis - by detecting
 PT mutations in alpha-mannosidase gene, also nucleic acid encoding the
 PT enzyme and derived oligo:nucleotide primers.
 XX PS Example 2; Page 22; 85pp; English.
 XX CC Forward primer mp5UTP is based on a 1500 bp amplicon produced from
 CC bovine fibroblast genomic DNA using primers (see AAT91098-99) based on
 CC the bovine alpha-mannosidase (LAMN) gene (see AAT91086). It was used
 CC with reverse primer mp262 (see AAT91101) to obtain an 800 bp RT-PCR
 CC product that constituted a 5' part of LAMN cDNA. This was combined with
 CC a previously obtained PCR cDNA fragment (see AAT91096-97) to produce a
 CC full-length clone (see AAT91086) for LAMN (see AAT26682). Mutations in
 CC the LAMN gene cause bovine alpha-mannosidosis, and can be detected using
 CC claimed PCR primers (see AAT91088-93)
 XX SQ Sequence 20 BP; 2 A; 5 C; 11 G; 2 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 2; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 378 GCGGCGGCTGCA 389
 Db 7 GCGGCGGCTGCA 18
 XX
 XX RESULT 246
 XX AAT9833
 XX ID AAT9833 standard; DNA; 20 BP.
 XX AC AAT9833;
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX OS WO9741258-A1.
 XX PN WO9741258-A1.
 XX PD 06-NOV-1997.
 XX PF 29-APR-1997; 97WO-US007134.
 XX PR 01-MAY-1996; 96US-00640672.
 XX PR 19-JUL-1996; 96US-00684498.
 XX PA (VIST-) VISIBLE GENETICS INC.
 XX PI Leushner J, Hui M, Dunn JM, Larson MT, Lacroix J;
 XX DR WPI; 1997-549754/50.
 XX PT Analysing nucleic acid containing sample - comprises performing multiplex
 PT amplification reaction and reacting amplified fragments in sequencing

PT reaction mixture.
 XX PS Example 4; Page 18; 37pp; English.
 XX CC This sequence represents a primer for exon 5 of the p53 gene. This
 CC sequence can be used in the method of the invention for analysing a
 CC nucleic acid containing sample. The method comprises performing a
 CC multiplex amplification reaction on the nucleic acids in the sample using
 CC amplification primer pairs, one pair for each region to be analysed, to
 CC produce a mixture of amplified fragments, and determining the sequence of
 CC at least one species of amplified fragment, characterised in that the
 CC sequence is determined by combining the mixture of amplification
 CC fragments with a sequencing reaction mixture for the production of
 CC sequencing fragments, and evaluating the sequencing fragments produced.
 CC The method can be used to analyse regions in the nucleic acids in the
 CC sample for the presence of mutations, or detect and type microorganisms.
 CC The method directly performs sequencing reactions on complex DNA mixtures
 XX SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 2; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 510 TCGTCTCTCCAG 521
 Db 9 TCGTCTCTCCAG 20
 XX
 XX RESULT 247
 XX AAT9834/C
 XX ID AAT9834 standard; DNA; 20 BP.
 XX AC AAT9834;
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX OS WO9741258-A1.
 XX PN WO9741258-A1.
 XX PD 06-NOV-1997.
 XX PF 29-APR-1997; 97WO-US007134.
 XX PR 01-MAY-1996; 96US-00640672.
 XX PR 19-JUL-1996; 96US-00684498.
 XX PA (VIST-) VISIBLE GENETICS INC.
 XX PI Leushner J, Hui M, Dunn JM, Larson MT, Lacroix J;
 XX DR WPI; 1997-549754/50.
 XX PT Analysing nucleic acid containing sample - comprises performing multiplex
 PT amplification reaction and reacting amplified fragments in sequencing
 PT reaction mixture.
 XX PS Example 4; Page 18; 37pp; English.
 XX CC This sequence represents a primer for exon 6 of the p53 gene. This
 CC sequence can be used in the method of the invention for analysing a
 CC nucleic acid containing sample. The method comprises performing a
 CC multiplex amplification reaction on the nucleic acids in the sample using
 CC amplification primer pairs, one pair for each region to be analysed, to
 CC produce a mixture of amplified fragments, and determining the sequence of

CC at least one species of amplified fragment, characterised in that the
 CC sequence is determined by combining the mixture of amplification
 CC fragments with a sequencing reaction mixture for the production of
 CC sequencing fragments, and evaluating the sequencing fragments produced.
 CC The method can be used to analyse regions in the nucleic acids in the
 CC sample for the presence of mutations, or detect and type microorganisms.
 CC The method directly performs sequencing reactions on complex DNA mixtures
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred.No.1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCCTCTCTCCAG 521
 |||||
 Db 18 TCCTCTCTCCAG 7

RESULT 248
 AAV47975
 ID AAV47975 standard; DNA; 20 BP.
 XX
 AC AAV47975;
 XX
 DT 19-OCT-1998 (first entry)
 XX
 DE Human B7-2 targeted oligonucleotide 10371.
 XX
 KM ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
 KM cell proliferation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 XX /note= "Phosphorothioate linkages"

PN MO9829124-A1.

PD 09-JUL-1998.

PF 16-DEC-1997; 97MO-US023270.

PR 31-DEC-1996; 96US-00777266.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Vickers TA;

DR WPI; 1998-387783/33.

PT New oligo:nucleotide(s) that modulate expression of B7 proteins - used
 PT for, e.g. controlling activation and proliferation of T cells,
 PT particularly for treatment, diagnosis and prevention of inflammation.
 XX
 PS Example 1; Page 38; 120pp; English.

XX The oligonucleotides which specifically hybridise to B7 modulate its
 CC expression (and thus T cell activation and proliferation). This is
 CC particularly useful for treatment and prevention of inflammation and
 CC autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
 CC Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
 CC (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
 CC rhinitis, allergy, cancer and metastases. The oligonucleotides may also
 CC be used to manipulate T cell activation ex vivo, to determine or detect
 CC B7 protein expression, for diagnosis, as assay and purification reagents,
 CC and to study physiological roles of B7 proteins
 XX
 SQ Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred.No.1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 TCCTGAGAGCCCC 258
 |||||
 Db 6 TCCTGAGAGCCCC 17

RESULT 249
 AAV55998
 ID AAV55998 standard; DNA; 20 BP.
 XX
 AC AAV55998;
 XX
 DT 04-DEC-1998 (first entry)
 XX
 DE GTPCH-1 mRNA amplifying RT-PCR primer 1gcl.

XX Selective inhibitor; nitric oxide synthase; NOS; tetrahydrobiopterin;
 KM THB; GTP cyclohydrolase 1; nitric oxide; septic shock; asthma; arthritis;
 KM inflammatory bowel disease; heart failure; acute systemic inflammation;
 KM neurological disease state; neuronal NOS; dementia; Parkinson's disease;
 KM stroke; RT-PCR; GTPCH-1; primer; ss.

OS Synthetic.
 OS Homo sapiens.

PN MO9835055-A1.

PD 13-AUG-1998.

PE 05-FEB-1998; 98MO-GB000353.

FR 05-FEB-1997; 97GB-00002312.

PA (UNIL) UNIV COLLEGE LONDON.

PI Charles IG, Bhagat K, Vallance PJT, Hingorani AD;

DR WPI; 1998-542240/46.

PT Identification of selective inhibitors of nitric oxide synthases - by
 PT determining inhibition of enzyme activity in presence of candidate
 PT compound and varying concentrations of tetrahydrobiopterin.

PS Example; Page 13; 30pp; English.

XX Sequences shown in AAV55996 to AAV56003 represent primers used for RT-PCR
 CC amplification during the course of the invention. The invention provides
 CC a method for identification of selective inhibitors of nitric oxide
 CC synthases (NOS) which comprises determining inhibition of activity of NOS
 CC in the presence of a candidate compound and two different concentrations
 CC of tetrahydrobiopterin (THB). Inhibitor of GTP cyclohydrolase 1-mediated
 CC synthesis of THB can be identified by contacting GTP cyclohydrolase 1
 CC with a candidate compound and determining inhibition of the enzyme
 CC mediated synthesis of THB by the candidate compound. The inhibitors
 CC identified by the methods may be used in treatment of conditions in which
 CC the production of nitric oxide (NO) is implicated, such as septic shock,
 CC asthma, arthritis, inflammatory bowel disease, heart failure or acute
 CC systemic inflammation. The inhibitors may also be useful in treatment of
 CC neurological disease states in which neuronal NOS has been implicated,
 CC e.g. stroke, dementia or Parkinson's disease
 XX

SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred.No.1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 TTGGTATCTTC 148
 |||||
 Db 1 TTGGTATCTTC 12


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RESULT 250
AAZ90365
ID AAZ90365 standard; DNA; 20 BP.
XX
AC AAZ90365;
XX
DT 24-SEP-1999 (first entry)
XX
DE Human p53 gene reverse transcription PCR primer exon 5 antisense.
XX
KM Human; p53; reverse transcription; PCR primer; resistance; mutant;
XX cancer; cyclin D1 protein; chemotherapy; cytotoxic; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN GB2334577-A.
XX
PD 25-AUG-1999.
XX
PF 18-FEB-1998; 98GB-00003446.
XX
PR 18-FEB-1998; 98GB-00003446.
XX
PA (UYLT-) UNIT LIVERPOOL.
XX
PI Warenus HM;
XX
DR WPI; 1999-422070/36.
XX
PT Measuring resistance of p53 mutant cancer cells to cytotoxic agents.
XX
PS Example; Page 13; 26pp; English.
XX
CC The present invention describes a method for measuring the resistance of
CC p53 mutant cancer cells to the cytotoxic effects of chemotherapeutic
CC agents by testing a sample comprising p53 mutant cells or an extract from
CC p53 mutant cells for the abundance of cyclin protein D1. AAZ90360 to
CC AAZ90373 represent reverse transcription PCR primers used to amplify the
CC human p53 gene. The method can be used to predict the response of human
CC cancer cells to anticancer therapy agents which can be used to select the
CC most appropriate therapy for patients suffering from cancer. High cyclin
CC D1 levels or high cyclin D1 expression together with p53 mutation is
CC strongly associated with resistance to cis-diaminedichloroplatinum (CDDP)
CC in human cancer cells. The test may be used to detect resistance to other
CC cytotoxic agents such as etoposide and indicate whether radiation may be
CC a viable alternative to CDDP or if other cytotoxic agents would be more
CC suitable, e.g. may suggest that Taxol should be considered as an
CC alternative therapy as it may not be sensitive to a combination of p53
CC mutation and cyclin D1 protein overexpression
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 510 TCCTCTCTCCAG 521
|||
DB 9 TCCTCTCTCCAG 20

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XX
KM G-alpha-13; human; inhibitor; cancer; antisense compound; therapy;
XX PCR primer; ss.
XX
OS Synthetic.
XX OS Homo sapiens.
XX
PN US5981732-A.
XX
PD 09-NOV-1999.
XX
PF 04-DEC-1998; 98US-00205860.
XX
PR 04-DEC-1998; 98US-00205860.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cowser LM;
XX
DR WPI; 1999-633376/54.
XX
PT Antisense compound inhibiting expression of human G-alpha-13.
XX
PS Example 14; Col 37; 38pp; English.
XX
CC This sequence represents a PCR primer for DNA encoding the human G-alpha-
CC 13 protein. The invention relates to an antisense compound of 8 to 30
CC nucleobases in length, that inhibits the expression of the human G-alpha-
CC 13. The antisense compound is useful for treating an animal, particularly
CC humans, having or being prone to a disease or condition associated with
CC the expression of G-alpha-13, such as cancer
XX
SQ Sequence 20 BP; 5 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 319 AGGATCTTCACC 330
|||
DB 9 AGGATCTTCACC 20

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RESULT 252
AAV80729/c
ID AAV80729 standard; DNA; 20 BP.
XX
AC AAV80729;
XX
DT 26-MAR-1999 (first entry)
XX
DE Alpha melanocyte-stimulating hormone receptor PCR primer BPIG13.
XX
KM Porcine; wild boar; meishan; pietrain; large white; hamshire; duroc;
XX differentiation; breed origin; alpha-MSHR; coat colour; stock purity;
XX alpha melanocyte-stimulating hormone receptor; KIT; PCR primer; ss.
XX
OS Synthetic.
OS Sus scrofa.
XX
PN W09854360-A1.
XX
PD 03-DEC-1998.
XX
PF 27-MAY-1998; 98WO-GB001531.
XX
PR 30-MAY-1997; 97GB-00011214.
XX
PR 31-JAN-1998; 98GB-00001190.
XX
PA (PIGT-) PIG IMPROVEMENT CO UK LTD.
XX
PI Andersson L, Kljase U, Giuffra E, Evans GJ, Wales R, Plastow GS;
XX

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DR WPI; 1999-070222/06.
XX
XX Differentiating products from different animal breeds - by the analysis
PT of alleles of breed-determinant genes, at the nucleic acid or protein
PT level.
XX
XX Example 22; Page 70; 101pp; English.
XX
XX A method has been developed for: (a) differentiating animals and animal
CC products according to breed origin; (b) determining or testing the breed
CC origin of a product; or (c) validating an animal product. The method
CC comprises analysing a sample of the product for the allele(s) of at least
CC one breed-determinant (BD) gene. The present invention also describes:
CC (i) methods for determining the coat colour genotype of a pig by
CC determining: (i) the allele(s) of the alpha melanocyte-stimulating
CC hormone receptor (alpha-MSHR) gene; (ii) the amino acid sequence of an
CC alpha-MSHR protein at positions associated with coat colour, or the size
CC of the protein; (iii) detecting which microsatellites (or other linked
CC marker alleles), linked to the alpha-MSHR gene, or particular alleles of
CC it, are present; and (iv) analysing nucleic acid to determine if the KIT
CC gene carries a polymorphism associated with the Belt genotype. The main
CC method of the invention is applied to samples from fish, birds and
CC mammals, especially pigs. Particular applications are confirming stated
CC origin of meats; in quality control; for maintaining stock purity, and in
CC breeding programmes (to confirm particular crosses). The method requires
CC only very small samples and many samples can be screened quickly and
CC inexpensively. The process can be made quantitative. The present sequence
CC represents an alpha-MSHR PCR primer from the present invention
XX
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 243 CACCTCTCTGAG 254
Db 20 CACCTCTCTGAG 9
RESULT 253
AA90393
ID AAX90393 standard; DNA; 20 BP.
XX
XX AAX90393;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX Human p53 gene reverse transcription PCR primer exon 5 antisense.
DE
XX Human; p53; reverse transcription; PCR primer; cancer; diagnosis; mutant;
KM cyclin-dependent kinase; CDK; ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX GB2334578-A.
PN
XX 25-AUG-1999.
PD
XX 18-FEB-1998; 98GB-00003447.
PF
XX 18-FEB-1998; 98GB-00003447.
PR
XX 18-FEB-1998; 98GB-00003447.
PA (UYLI-) UNIV LIVERPOOL.
XX
XX Warrenius HM; Seabra L;
PI
XX WPI; 1999-432548/37.
DR
XX
XX
PT Diagnosis of cancerous or pre-cancerous cells by monitoring the levels of
PT cyclin-dependent kinases 1 and 4.
XX

PS Example; Page 12; 26pp; English.
XX
XX The present invention describes a method for the diagnosis of a cancerous
CC or pre-cancerous state from the co-elevation of cyclin-dependent kinase 1
CC (CDK1) and CDK4 levels. The method may be used for the clinical diagnosis
CC of cancerous or pre-cancerous cells. In addition the combination of
CC targets may be used to screen for drugs that may specifically act on
CC cancer cells. The combination of CDK1, CDK4 elevation and p53 mutation in
CC combination form a complex target that is likely to be specific for
CC cancerous cells. AAX90388 to AAX90401 represent reverse transcription PCR
CC primer for the human p543 gene, used in an example from the present
XX invention
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 2.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 510 TCGTCTCTCCAG 521
Db 9 TCGTCTCTCCAG 20
RESULT 254
AA90379
ID AAX90379 standard; DNA; 20 BP.
XX
XX AAX90379;
AC
XX
XX 24-SEP-1999 (first entry)
DT
XX
XX Human p53 gene reverse transcription PCR primer exon 5 antisense.
DE
XX Human; p53; reverse transcription; PCR primer; cancer; cytotoxic;
KM signal transduction factor; mutant; cell cycle; apoptosis; chemotherapy;
KM ss.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX GB2334579-A.
PN
XX 25-AUG-1999.
PD
XX 03-JUL-1998; 98GB-00014545.
PF
XX 18-FEB-1998; 98GB-00003446.
PR 18-FEB-1998; 98GB-00003447.
PR 05-JUN-1998; 98GB-00012151.
XX
XX (UYLI-) UNIV LIVERPOOL.
PA (THER-) THERYTE LTD.
XX
XX Warrenius HM; Seabra LA;
PI
XX WPI; 1999-442071/36.
DR
XX
XX
PT Determination of sensitivity of cancer cells to anti-cancer agents.
PS
XX Example 1; Page 18; 46pp; English.
XX
XX The present invention describes a method for the determination of
CC sensitivity of cancer cells to anti-cancer agents by measuring the
CC mutational status, expression and/or function of signal transduction
CC factors. The method, by measuring the resistance of cells to anti-cancer
CC agents, is useful for selecting the most appropriate therapy for patients
CC suffering from cancer. AAX90374 to AAX90387 represent reverse
CC transcription PCR primer for the human p543 gene, used in an example from
CC the present invention
XX
SQ Sequence 20 BP; 2 A; 9 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 510 TCGTCTCTCCAG 521
 |||||
 DB 9 TCGTCTCTCCAG 20

RESULT 255
 AAZ00491
 ID AAZ00491 standard; DNA; 20 BP.
 XX
 AC AAZ00491;
 XX
 DT 06-OCT-1999 (first entry)
 XX
 DE Human thiorredoxin DNA binding antisense oligonucleotide 2614.
 XX
 KM Thiorredoxin; thiorredoxin reductase; human; antisense; primer; metastasis;
 KM cytoskeletal; tumour growth inhibitor; detection; nuclease resistant;
 KM phosphorothioate linkage; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO938963-A1.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JUN-1999; 99WO-CA000077.
 XX
 PR 30-JAN-1998; 98US-0073196P.
 XX
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PI Wright JA, Young AH, Lee YS;
 PI WPI; 1999-469328/39.
 XX
 DR WPI; 1999-469328/39.
 XX
 PT Antisense oligonucleotides against thiorredoxin and thiorredoxin reductase
 XX gene, useful for inhibiting tumor growth and metastasis.
 XX
 PS Claim 1; Page 18; 88pp; English.
 XX
 CC This invention describes novel antisense oligonucleotides against
 CC thiorredoxin and thiorredoxin reductase gene which have cytoskeletal activity
 CC and are useful for inhibiting tumor growth and metastasis in mammals.
 CC They may also be used as hybridization probes to detect the presence of
 CC the thiorredoxin and thiorredoxin reductase mRNAs in mammalian cells. They
 CC may also be used as molecular weight markers. The antisense
 CC oligonucleotides are nuclease resistant due to the presence of
 CC phosphorothioate internucleotide linkages. AAZ00478-Z00503 represent
 CC oligonucleotide primers capable of binding to human thiorredoxin mRNA
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 442 TCGAATACTTTT 453
 |||||
 DB 7 TCGAATACTTTT 18

RESULT 256
 AAX79784
 ID AAX79784 standard; DNA; 20 BP.
 XX
 AC AAX79784;
 XX
 DT 17-AUG-1999 (first entry)

XX
 DE PCR primer H16016 for mitochondrial DNA analysis.
 XX
 KM PCR primer; human; mitochondrial DNA; genetic diagnosis;
 KM adult disease contraction; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN JP11113597-A.
 XX
 PD 27-APR-1999.
 XX
 PF 13-OCT-1997; 97JP-00279127.
 XX
 PR 13-OCT-1997; 97JP-00279127.
 XX
 PA (TANAKA/) TANAKA M.
 XX
 DR WPI; 1999-320841/27.
 XX
 PT Genetic diagnosis using human mitochondrial DNA - comprises detecting
 PT base replacements.
 XX
 PS Example 2; Page 6; 15pp; Japanese.
 XX
 CC This sequence represents a PCR primer that can be used in the method of
 CC the invention. The method is for genetic diagnosis using human
 CC mitochondrial DNA where there is at least one base replacement from among
 CC the following five replacements: the 3010th base is changed from guanine
 CC to adenine; the 4883rd base from cytosine to thymine; the 5178th base
 CC from cytosine to adenine; the 8414th base from cytosine to thymine; and
 CC the 1468th base from cytosine to thymine. The method can be used for
 CC diagnosing the probability of contracting adult diseases. A confirmation
 CC of base replacement can give a diagnosis of the level of probability of
 CC contraction of adult diseases
 XX
 SQ Sequence 20 BP; 10 A; 4 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 462 CCATGAAGAGAC 473
 |||||
 DB 2 CCATGAAGAGAC 13

RESULT 257
 AAX92037
 ID AAX92037 standard; DNA; 20 BP.
 XX
 AC AAX92037;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 KM Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
 KM sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
 KM neutralising epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 PN WO9927105-A2.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-IB001890.
 XX
 PR 21-NOV-1997; 97FR-00014673.
 XX
 DT 04-NOV-1998; 98US-0107078P.

```

XX (GEST ) GENSET.
XX
XX Grifflais R;
XX
XX WPI; 1999-357842/30.
XX
XX Genome sequence of Chlamydia pneumoniae.
XX
XX Page 1480; Disclosure; 1912pp; English.
XX
XX AAX91991.X97517 represent PCR primers used to amplify open reading frames
XX and other nucleic acid sequences from the genome of Chlamydia pneumoniae
XX (see AAX91990). C. pneumoniae causes respiratory disease such as
XX pneumonia and bronchitis and is thought to be a contributing factor in
XX heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
XX nodosum or pharyngitis. The polypeptides encoded by the open reading
XX frames of the C. pneumoniae genome (see AAY34584 - AAY35879) can be used
XX in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
XX nucleotide sequences can also be used as immunogenic compositions,
XX especially where the vector directs the expression of a neutralising
XX epitope of C. pneumoniae
XX
XX Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 2; Length 20;
XX Best Local Similarity 100.0%; Pred.No.1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 316 CTGAGATCTTC 327
DB 9 CTGAGATCTTC 20

```

RESULT 258

AAC61817/C

ID AAC61817 standard; DNA; 20 BP.

AC AAC61817;

XX

DT 06-MAR-2001 (first entry)

XX

DE Antisense oligonucleotide directed against human Fas (Apo-1) gene.

XX

KW Human; Fas; Apo-1; antisense compound; Fas ligand; Fas-1; hepatitis;

KW Fas associated protein 1; protein tyrosine phosphatase; cancer;

KW autoimmune disease; inflammatory disease; lymphoma; phosphorothioate; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT misc_feature 1..20

FT /*tag= b

FT /note= "contains phosphorothioate linkages"

FT modified_base 1..5

FT /*tag= a

FT /note= "2'-methoxyethoxy residues"

FT modified_base 16..20

FT /*tag= c

FT /note= "2'-methoxyethoxy residues"

XX

PN WO200061150-A1.

XX

PD 19-OCT-2000.

XX

PF 10-APR-2000; 2000WO-US009540.

XX

PR 12-APR-1999; 99US-00290640.

XX

PA (ISIS-) ISIS PHARM INC.

XX

PI Dean NM, Marcusson Eg;

```

XX WPI; 2000-628395/60.
XX
XX Antisense oligonucleotides for treating hepatitis and colon, liver or
XX lung cancer are inhibitors of Fas, Fas ligand or Fas associated protein 1
XX (Fas-1) expression.
XX
XX Claim 3; Page 45; 116pp; English.
XX
XX AAC61799-C61819 represent antisense oligonucleotides which are directed
XX against nucleic acid compounds encoding human Fas (Apo-1). The specification
XX describes antisense compounds which are targeted to the 5'-untranslated
XX region, translational start site, translational termination region or 3'-
XX untranslated region of nucleic acid molecules encoding Fas, Fas ligand
XX (FasL), or Fas-1 (Fas associated protein 1, protein tyrosine
XX phosphatase). The antisense compounds are used to inhibit the expression
XX of Fas, FasL or Fas-1 in cells or tissues. They are used to treat
XX autoimmune or inflammatory diseases such as hepatitis. They can also be
XX used to treat cancer, especially colon, liver or lung cancer or lymphoma
XX
XX Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 3; Length 20;
XX Best Local Similarity 100.0%; Pred.No.1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 171 GGAATTCCTCT 182
DB 20 GGAATTCCTCT 9

```

RESULT 259

AAA37589

ID AAA37589 standard; DNA; 20 BP.

AC AAA37589;

XX

DT 15-AUG-2000 (first entry)

XX

DE Antisense sequence #47 used to inhibit telomerase activity.

XX

KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;

KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;

KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;

KW paternity testing; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

XX Key Location/Qualifiers

FT misc_feature 1..20

FT /*tag= a

FT /note= "Phosphorothioate internucleotide linkages"

XX

PN US6046307-A.

XX

PD 04-APR-2000.

XX

PF 09-APR-1997; 97US-00838545.

XX

PR 09-APR-1996; 96US-00630019.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;

XX

DR WPI; 2000-292432/25.

XX

PF New peptide nucleic acid (PNA) compounds that inhibit telomerase activity

PT in mammalian cells is useful as probes to detect the RNA component of a

XX mammalian telomerase.

XX

PS Example 1; Col 29; 45pp; English.

The present sequence represents an antisense oligonucleotide used as a control sequence alongside a peptide nucleic acid molecule which as a hybridizes to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands, and increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase RNA (hTR) sequence. PNA probes are also used for forensic identification of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

319 AGGATCTTCACC 330
1 AGGATCTTCACC 12

RESULT 260
AAA37584
AAA37584 standard; DNA; 20 BP.

15-AUG-2000 (first entry)

PNA sequence #42 used to inhibit telomerase activity.

Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer; inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia; AIDS; HIV; fungal infection; forensic identification; detect; tumour; paternity testing; ss.

Synthetic.

Key Location/Qualifiers
misc_feature 1..20

/note= "Peptide nucleic acid molecule, where N-(2-aminoethyl)glycine units are linked to nucleotide bases via glycine amino N through a methylenecarbonyl linker"

US6046307-A.

04-APR-2000.

09-APR-1997; 97US-00838545.

09-APR-1996; 96US-00630019.
(TEXA) UNIV TEXAS SYSTEM.
Wright WR, Piatyzek MA, Shay JW, Norton JC, Corey DR;
WPI; 2000-292432/25.
New peptide nucleic acid (PNA) compounds that inhibit telomerase activity in mammalian cells is useful as probes to detect the RNA component of a mammalian telomerase.
Example 1; Col 27-28; 45pp; English.
The present sequence represents a peptide nucleic acid molecule which hybridizes to the mRNA component of mammalian telomerase, and inhibits telomerase activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one strand of the telomeric DNA, using as a template an 11 nucleotide sequence contained within the RNA component of the enzyme. The invention relates to PNA molecules having a sequence of no more than 25 bases, which include the sequence GTTAGG. The uncharged nature of the PNA backbone increases the melting temperature of associating strands, and increases the rate of association with targeted nucleic acids, and affords greater resistance of degradation by proteases or nucleases. The therapeutic PNAs may be used for treating disease conditions such as cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency syndrome) and associated pathologies, fungal infections, and other diseases characterized by abnormal telomere metabolism or telomerase activity, in combination with antineoplastic and other cytotoxic or cytostatic agents, antifungal agents, and other nucleotides. PNAs may be used for molecular diagnostics, labelled PNAs are used as hybridization probes to detect or quantitate polynucleotides having a human telomerase RNA (hTR) sequence. PNA probes are also used for forensic identification of individuals, e.g. paternity testing, based on hTR gene restriction fragment length polymorphism (RFLP) pattern. PNAs are also useful as probes to detect the RNA component of a mammalian telomerase and as inhibitors of telomerase activity. The method of the present invention allows cancerous conditions to be detected with increased confidence and possibly at an earlier stage, before cells are detected as cancerous based on pathological characteristics. The diagnostic and prognostic methods of the present invention can be used to detect an immortal or neoplastic cell or tumour tissue or cancer of any origin, provided the cell expresses telomerase activity and its RNA component

Query Match 2.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

319 AGGATCTTCACC 330
1 AGGATCTTCACC 12

RESULT 261
AAZ77376/c
AAZ77376 standard; DNA; 20 BP.

AAZ77376;

10-SEP-2001 (first entry)

Human biallelic marker downstream amplification primer SEQ ID NO:11732.

Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic bases; genotyping; haplotyping; hybridisation; identification; characterization; amplification; single nucleotide polymorphism; SNP; PCR primer; diagnosis; ss.

Homo sapiens.

XX WO954500-A2.
 XX 28-OCT-1999.
 XX
 XX 21-APR-1999; 99WO-IB000822.
 XX 21-APR-1998; 98US-0082614P.
 XX 23-NOV-1998; 98US-0109732P.
 XX
 XX (GENSET) GENSET.
 XX Cohen D, Blumenfeld M, Chumakov I;
 XX WPI; 2000-013267/01.
 XX
 XX Novel biallelic markers used to construct a high density disequilibrium
 XX map of the human genome.
 XX
 XX Claim 9; Page 2731; 2745pp; English.
 XX
 XX AA265654 to AA269578 represent human biallelic markers from the present
 XX invention, which contain a polymorphic base at position 24 of their
 XX nucleotide sequences. AA269579 to AA277440 represent amplification
 XX primers for the biallelic markers. The biallelic markers of the invention
 XX have a variety of uses: they can be used for high density mapping of the
 XX human genome, and in complex association studies and haplotyping studies
 XX which are useful in determining the genetic basis for disease states.
 XX Compositions and methods of the invention can also be useful for the
 XX identification of the targets for the development of pharmaceutical
 XX agents and diagnostic methods, as well as the characterisation of the
 XX differential efficacious responses to and side effects from
 XX pharmaceutical agents acting on a disease as well as other treatment.
 XX N.B. The SEQ ID NOS 2852, 2813, 2974, 3035, 3086, 3157, 3227, 3297 and
 XX 3367, are not actually given a sequence in the Sequence Listing from the
 XX present invention
 XX
 XX Sequence 20 BP; 6 A; 2 C; 9 G; 3 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 3; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 511 CGTCTCTCCAGA 522
 XX 14 CGTCTCTCCAGA 3
 XX
 XX RESULT 262
 XX AA247037
 XX ID AA247037 standard; DNA; 20 BP.
 XX
 XX AC AA247037;
 XX
 XX 15-MAR-2000 (first entry)
 XX
 XX Primer #2 for human beta-actin gene.
 XX
 XX Antiviral; anticancer; antiproliferative; human; interferon-alphas;
 XX hepatic disease; hepatitis C; viral cirrhosis; hepatocellular carcinoma;
 XX liver; gene expression; primer; PCR; amplification; beta-actin; ss.
 XX
 XX Synthetic.
 XX Homo sapiens.
 XX
 XX WO958143-A1.
 XX
 XX 18-NOV-1999.
 XX
 XX 13-MAY-1999; 99WO-ES000134.
 XX
 XX 13-MAY-1998; 98BS-00001003.
 XX

PA (CIEN-) INST CIENTIFICO & TECNOLOGICO NAVARRA.
 XX Prieto Valtuena J, Civeira Murillo MP, Larrea Leoz E;
 XX WPI; 2000-038959/03.
 XX
 XX Treating liver diseases with interferon-alphas or nucleic acid encoding
 XX it, particularly chronic hepatitis C.
 XX
 XX Disclosure; Page 11; 36pp; Spanish.
 XX
 XX The invention relates to a method of using interferon-alphas or its
 XX coding sequence to prepare compositions for treatment of hepatic
 XX diseases, e.g. (i) chronic hepatitis C; (ii) cirrhosis of viral origin
 XX and (iii) hepatocellular carcinoma. The method restores the level of
 XX interferon-alphas, which is reduced in diseased liver cells, to normal
 XX levels. The primers AA247036-247037 were used initially to detect the
 XX level of expression of beta-actin gene in liver tissue by PCR as a
 XX control for detecting the level of interferon-alpha or beta. The primers
 XX amplify a 314 bp fragment of the human beta-actin gene
 XX
 XX Sequence 20 BP; 4 A; 2 C; 8 G; 6 T; 0 U; 0 Other;
 XX
 XX Query Match 2.0%; Score 12; DB 3; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 317 TGAGGATCTTCA 328
 XX 3 TGAGGATCTTCA 14
 XX
 XX RESULT 263
 XX AA66151/C
 XX ID AA66151 standard; DNA; 20 BP.
 XX
 XX AC AA66151;
 XX
 XX 09-OCT-2000 (first entry)
 XX
 XX Dog genomic marker oligonucleotide sequence SEQ ID NO:13.
 XX
 XX Dog; genome; genomic marker; radiation hybrid map; identification;
 XX chromosome location; gene marker; polymorphic microsatellite marker;
 XX phenotype; behaviour; pedigree; ss.
 XX
 XX Canis familiaris.
 XX
 XX WO200029615-A2.
 XX
 XX 25-MAY-2000.
 XX
 XX 15-NOV-1999; 99WO-IB001907.
 XX
 XX 13-NOV-1998; 98US-0108193P.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 XX
 XX Gallibert F, Andre C;
 XX WPI; 2000-387821/33.
 XX
 XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
 XX for e.g. identifying genes implicated in phenotypic and behavioral traits
 XX or in genetic diseases and for studying dog pedigrees.
 XX
 XX Claim 1; Page 53; 87pp; English.
 XX
 XX The present invention describes a radiation hybrid map of the dog (Canine
 XX familiaris) genome comprising the genome location of a marker selected
 XX from AA66139 to AA66942. The radiation hybrid map is useful for
 XX identifying and localising dog genes, since it covers approximately 80 %
 XX of the dog genome and provides a dense map integrating different types

(i.e. Type I and Type II) of markers. The map and the dog genome markers (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioral traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases

Sequence 20 BP; 2 A; 10 C; 2 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 2.0%; Score 12; DB 3; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

486 GGAGGCGCTGCA 497

17 GGAGGCGCTGCA 6

RESULT 264

AAAF33001 standard; DNA; 20 BP.

AAAF33001;

23-MAR-2001 (first entry)

Human B7-2 antisense oligonucleotide SEQ ID NO: 198.

Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;

autoimmune disorder; phosphorothioate backbone; ss.

Homo sapiens.

MO200074687-A1.

14-DEC-2000.

25-MAY-2000; 2000WO-US014471.

04-JUN-1999; 99US-00326186.

(ISIS-) ISIS PHARM INC.

Bennett CF, Vickers TA, Karas JG;

WPI; 2001-049991/06.

Novel compound for diagnosing, preventing and treating immune disorders, comprising an oligonucleotide that specifically hybridizes with a nucleic acid sequence encoding B7 protein.

Example 14; Page 84; 162pp; English.

The present invention provides sequences of antisense oligonucleotides targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences. The antisense sequences have phosphorothioate backbones and some nucleotides are 2'-methoxyethoxy residues. The sequences can be used in the treatment of inflammatory and autoimmune disorders, including asthma, juvenile diabetes mellitus, myasthenia gravis, Graves' disease, rheumatoid arthritis, allograft rejection, inflammatory bowel disease, multiple sclerosis, psoriasis, systemic lupus erythematosus, contact dermatitis, rhinitis, allergies and cancer

Sequence 20 BP; 3 A; 7 C; 6 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 2.0%; Score 12; DB 4; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 TCCTGGAGCCCC 258

5 TCCTGGAGCCCC 16

RESULT 265

AAAF32817 standard; DNA; 20 BP.

AAAF32817;

23-MAR-2001 (first entry)

Human B7-2 mRNA antisense oligonucleotide SEQ ID NO: 14.

Human; mouse; B7-1; B7-2; antisense; PCR primer; inflammation;

autoimmune disorder; phosphorothioate backbone; ss.

Homo sapiens.

MO200074687-A1.

14-DEC-2000.

25-MAY-2000; 2000WO-US014471.

04-JUN-1999; 99US-00326186.

(ISIS-) ISIS PHARM INC.

Bennett CF, Vickers TA, Karas JG;

WPI; 2001-049991/06.

Novel compound for diagnosing, preventing and treating immune disorders, comprising an oligonucleotide that specifically hybridizes with a nucleic acid sequence encoding B7 protein.

Example 1; Page 50; 162pp; English.

The present invention provides sequences of antisense oligonucleotides targeted at the murine and human B7-1 and B7-2 coding and mRNA sequences. The antisense sequences have phosphorothioate backbones and some nucleotides are 2'-methoxyethoxy residues. The sequences can be used in the treatment of inflammatory and autoimmune disorders, including asthma, juvenile diabetes mellitus, myasthenia gravis, Graves' disease, rheumatoid arthritis, allograft rejection, inflammatory bowel disease, multiple sclerosis, psoriasis, systemic lupus erythematosus, contact dermatitis, rhinitis, allergies and cancer

Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 2.0%; Score 12; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.2e+05; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

247 TCCTGGAGCCCC 258

6 TCCTGGAGCCCC 17

RESULT 266

AAAS15460 standard; DNA; 20 BP.

AAAS15460;

14-FEB-2002 (first entry)

Phosphorothioate (PS) oligomer IV used to inhibit telomerase activity.

Mammalian; forensic; paternity testing; human telomerase RNA component; hhr gene RFLP pattern; cancer; inflammation; lymphoproliferative disease; autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS; human immunodeficiency virus; telomere metabolism; mutant; acquired immunodeficiency syndrome; cytostatic; anti-inflammatory;

```

KM immunosuppressive; phosphorothioate; ss.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /label= OTHER
FT /note= "phosphorothioate internucleotide linkages"
XX US6294650-B1.
XX 25-SEP-2001.
XX 08-JUL-1999; 99US-00349532.
XX 09-APR-1996; 96US-00630019.
XX 09-APR-1997; 97US-00838545.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Shay JW, Wright WE, Platyszczek MA, Corey DR, Norton JC.
XX WPI; 2001-638024/73.
XX
XX New peptide nucleic acid that hybridizes to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases.
XX
XX Example 1; Col 29; 46bp; English.
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridizing to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component of
XX mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase RNA
XX component (hTR) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the hTR gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents a phosphorothioate (PS)
XX oligomer used to inhibit telomerase activity in the methods of the
XX present invention.
XX
XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 4; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 319 AGGATCTTCACC 330
XX |||||
XX 1 AGGATCTTCACC 12
XX
XX RESULT 267
XX AAS15455 standard; DNA; 20 BP.
XX
XX AAS15455;
XX
XX 14-FEB-2002 (first entry)
XX
XX PNA XIV inhibiting human and mammalian telomerase activity.
XX
XX DE

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```

XX KM Mammalian; peptide nucleic acid; probe; forensic; paternity testing;
XX KM human telomerase RNA component; hTR gene RFLP pattern; cancer;
XX KM inflammation; lymphoproliferative disease; autoimmune disease;
XX KM neurodegenerative disease; neoplasia; hyperplasia; HIV; AIDS;
XX KM human immunodeficiency virus; acquired immunodeficiency syndrome;
XX KM telomere metabolism; mutant; cytostatic; anti-inflammatory;
XX KM immunosuppressive; polyamide backbone; ss.
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /note= "This sequence is a peptide nucleic acid, i.e. it
FT contains a polyamide backbone instead of a deoxyribose
FT backbone"
XX US6294650-B1.
XX 25-SEP-2001.
XX 08-JUL-1999; 99US-00349532.
XX 09-APR-1996; 96US-00630019.
XX 09-APR-1997; 97US-00838545.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Shay JW, Wright WE, Platyszczek MA, Corey DR, Norton JC.
XX WPI; 2001-638024/73.
XX
XX New peptide nucleic acid that hybridizes to the RNA component of
XX mammalian telomerase, useful for treating or preventing cancer,
XX inflammation, lymphoproliferative diseases, autoimmune disease, or
XX neurodegenerative diseases.
XX
XX Example 1; Col 29; 46bp; English.
XX
XX The present invention relates to peptide nucleic acids (PNAs), comprising
XX a sequence of 6-25 nucleobases, that inhibit telomerase activity in
XX mammalian cells by hybridizing to the RNA component of mammalian
XX telomerase. The PNAs are useful as probes to detect the RNA component of
XX mammalian telomerase and as inhibitors of telomerase activity, or to
XX detect and/or quantitate polynucleotide having the human telomerase RNA
XX component (hTR) sequence, as well as in forensic identification of
XX individuals, such as paternity testing or identification of criminal
XX suspects or unknown descendants based on the hTR gene RFLP pattern. The
XX PNA can be further used for treating or preventing cancer, inflammation,
XX lymphoproliferative diseases, autoimmune disease, or neurodegenerative
XX diseases. The PNAs in combination with other pharmaceuticals (such as
XX antineoplastic or cytostatic agents) can be used for treating neoplasia,
XX hyperplasia, human immunodeficiency virus (HIV) infections, acquired
XX immunodeficiency syndrome (AIDS) and associated pathologies, and other
XX diseases characterised by abnormal telomere metabolism or telomerase
XX activity. The present sequence represents one of the PNA sequences of the
XX present invention.
XX
XX Sequence 20 BP; 5 A; 6 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 2.0%; Score 12; DB 4; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.2e+05;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 319 AGGATCTTCACC 330
XX |||||
XX 1 AGGATCTTCACC 12
XX
XX RESULT 268
XX AAH75831

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